```
NAME: Steffe, Etic K.

REGISTRATION NUMBER: 36,688
REPERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
ITELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
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RESULT 1
   Sequence 4, Appliseduce 7652, Appliseduce 5, Appliseduce 5, Appliseduce 2, Appliseduce 2, Appliseduce 2, Appliseduce 1, Appliseduce 1, Appliseduce 2, Appliseduce 25, Appliseduce 25, Appliseduce 25, Appliseduce 25, Appli
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Sequence 4, Appli
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| /cgn2 / /cyn2 / /cyn2 / /cyn2 / /cyn2 
                                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-153-927-2
US-09-555-918-5
US-08-928-069-10
US-09-557-908-4
US-09-557-908-4
US-09-333-966-4
US-09-333-966-4
US-09-448-868-5
US-09-13-895A-5
US-09-13-895A-5
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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        Sequence
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APPLICANT: Ni, Jian
APPLICANT: Dilt, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Golderate
CTTM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.: 1100 New York Ave., NW, Suite 600
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUUNTEY: USA

ZIP: 20005-3934

COUNTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: US/08/815,885
FILING DATE: US/08/815,285
FILING DATE: US/08/815,285
FILING DATE: US/08/815,285
FILING DATE: US/08/815,285
                                                                           US-09-565-918-4
US-09-573-986-3
US-09-252-6568-3
US-09-252-6568-3
US-09-55-908-5
US-09-55-908-5
US-09-874-56-854-5
US-09-874-946-7
US-09-874-862-37
US-09-874-862-37
US-09-949-016-7946
US-09-949-016-7946
US-09-786-858-24
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   121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ### Sequence 5, Application US/09565918

### Sequence 5, Application US/09565918

### Patent No. 6433147

### GENERAL INPORMATION:

### APPLICANT: Ni, Jian

### APPLICANT: Rosen, Craig A.

### APPLICANT: Pan, James G.

### APPLICANT: Pan, James G.

### APPLICANT: Pan, James G.

### APPLICANT: Dixit, Vishva M.

### TITLE OF INVENTION: Death Domain Containing Receptor 4

### FILE REFERENCE: 1488.130000

### TITLE OF INVENTION: Death Domain Containing Receptor 4

### FILE REFERENCE: 1488.13000-05-05

### CURRENT APPLICATION NUMBER: US 60/132,922

### PRIOR PILING DATE: 1999-05-06

### PRIOR PILING DATE: 1999-01-27

### PRIOR PILING DATE: 1998-01-27

### PRIOR PILING DATE: 1998-01-27

### PRIOR PILING DATE: 1997-02-05

### PRIOR PILING DATE: 199
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Matches 417; Conservative
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Sequence 2, Application US/09153927A

Patent No. 6297022

GENERAL INFORMATION:

APPLICANT: McDonnell, Peter C.

APPLICANT: Young, Peter R.

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3

TITLE OF INVENTION: Antagonists for Mindows Version 3.0
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                                                                                                 Best Local Similarity 100.
Matches 417, Conservative
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                      DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLRBAE 360
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                                                                                                                                     361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERWGLDGCVEDLRSRLQRGF 417
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                                                                                                                                                                                                                                                                         Sequence 6, Application US/08828683A
Patent No. 646914
GENERAL INFORMATION—
APPLICANT ABINEMATA
TILLE OF INVENTION—AD0-2 LI AND AD0-3 FOLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS: 7
ADDRESSEE (Genentech, Inc.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94080

COMPUTER READABLE FORM:
COMPUTER: 15.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: MAXE: MAXECHARYON NUMBER: 35,600
REGISTRATION NUMBER: 35,600
TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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STATE: California
COUNTRY: USA
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TYPE: Amino Acid
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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                                                                                                                              361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVXAALERWGLDGCVEDLRSRLQRGP 417
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100.0%; Pred. No. 1.1e-193;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94080
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUW TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winheatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                            US-08-928-069-10

Sequence 10, Application US/08928069

Patent No. 646216

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-3 POLYPEPTIDE

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATION NUMBER: 60/026943
FILING DATE: 09/23/1996
ATTONEN'AGENT INPORMATION:
NAME: MARSCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REGISTRATION NUMBER: 35,600
REGISTRATION NUMBER: 91052R1
TELECOMMUNICATION INPORMATION:
TELEPHONE: 650/225-5416
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS;
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Amino Acid
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Best Local Similarity
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                                                                                                                                                                                                                                                             Sequence 5, Application US/09874138

Patent No. 6743625

GENERAL INPORMATION:
APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
TITLE GEINVENTION: Death Domain Containing Receptor 5
TITLE REFERENCE: 1488.1310006
CURRENT APPLICATION NUMBER: US/09/874,138
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/565,009
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR PILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/132,498
PRIOR FILING DATE: 1999-03-17
PRIOR FILING DATE: 1997-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100. Matches 417; Conservative
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ORGANISM: Homo sapiens
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                            MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
                                                         DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
                                                                                                                                                                        CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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Patent No. 6713061

Sequence 4, Application US/09557908

Patent No. 6713061

APPLICANT: Wi. Guo-Liang

APPLICANT: Ni. Jian

APPLICANT: Dillon, Patrick J.

APPLICANT: Dillon, Patrick J.

TILE OF INVENTION: Death Domain Containing Receptors

FILE REFERENCE: 1488 0310008

CURRENT FILING DATE: 1080-04-21

PRIOR FILING DATE: 1999-05-28

PRIOR PLICATION NUMBER: US 60/136,741

PRIOR FILING DATE: 1999-04-22

PRIOR FILING DATE: 1999-04-22

PRIOR FILING DATE: 1999-04-22

PRIOR FILING DATE: 1997-02-11

PRIOR PLICATION NUMBER: US 60/037,341

PRIOR PLING DATE: 1997-02-06

PRIOR PLING DATE: 1996-10-17

PRIOR PRIOR PLING DATE: 1996-10-17

PRIOR PLING DATE: 1996-10-17

PRIOR PRIOR PLING DATE: 1996-10-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 762. Application US/09949016
; Sequence 762. Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REFERENCE: CLOO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR PELLING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 CTEPCGNSTCLVCPQDTFLAMENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 149
                                                                                                                                           241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
                                                                                                                                                                                                    DQLPSRALGPAAAPTLSPESPAGSPAMIQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
                                                                                                                                                                                                                                                   301 DOLPSRALGPAAPTLSPESPAGSPAMIQPGPOLYDVMDAVPARRWKEFVRTLGLREAE 360
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                                                                                                       241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity 100.
417; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Human
US-09-949-016-7652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Si
Matches 417,
                                                                                                                                                                                                       301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEQRPRGCAAVAAALLIVILGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C. STREET: 1100 New York Ave., NW, Suite 600 CITY: Washington
                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Gentz, Reiner L.
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA

ZIP: 2005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: 05-8213 Yet Assigned
FILING DATE: 06-821997
FILING DATE: 06-821997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
PRIOR DATE: 17-0CT-1996
PRIOR DATE: 12-0AR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Bric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 2323; DB 4; Best Local Similarity 100.0%; Pred. No. 1.1e-193; Matches 417; Conservative 0; Mismatches 0;
                                                                           RESULT 8
US-09-313-966-4
; Sequence 4, Application US/09333966
; Patent No. 6759513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 417 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-09-333-966-4
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CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
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                                                                     1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pan, James G.
APPLICANT: Pan, James G.
APPLICANT: Pan, James G.
APPLICANT: Bentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
NUMBER OF SEGUENCES:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 833;
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COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
CURRENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/09/448,868
FILING DATE: HEREWITH
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/013,895
FILING DATE: 27-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1300004
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECHOME: (202) 371-2600
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100.0%; Pred. No. 2.7e-193;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: HUMAN GENOME SCIENCES, INC.: 9410 KEY WEST AVENUE ROCKVILLE
                                                                                                                                                                                                                                  Sequence 5, Application US/09448868; Patent No. 6461823; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 833 amirc TVOE
                                                                                                                                                                                                                                                                                                APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
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amino acid
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417; Conserva
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                                                                                                                                                                                                             US-09-448-868-5
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Best Local S
Matches 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADDEAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEQRPRGCAAVAAALLLVILGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP 60
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                                                                                   Sequence 5, Application US/09013895A
Patent No. 6342363
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
APPLICANT: Pan, James G.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Beath Domain Containing Receptor 4 (DR4: Death TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/013,895A
FILING DATE: 27-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 2323; DB 3;
100.0%; Pred. No. 2.7e-193;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: HUMAN GENOME SCIENCES, INC
STREET: 9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K,
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1300002
TELECOMMUNICATION INFORMATION:
TELEPONE: (202) 371-2600
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 417; Conservative 0
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LENGTH: 833 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                        ROCKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΩS
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                                          RESULT 10
US-09-013-895A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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                                                                                                                                                              68 LKAPCTEPCGNSTCLVCPODIFLAWENHHNSECARCOACDEOASOVALENCSAVADTRCG 127
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                                                8 EAPRGOLRGESAAPVPQALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHY
                                                                                                                                                                                                                                                                                                                                VSCPTSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTA
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     QRPRG-----CAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHY
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GENERAL TWOORWARTON:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Dilan, Vishva
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
FILE REFERENCE: 1488.0310008
CURRENT APPLICATION NUMBER: US/09/557,908
CURRENT APPLICATION NUMBER: US 60/136,741
PRIOR PELING DATE: 1999-05-28
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1997-02-06
PRIOR PELICATION NUMBER: US 60/037,341
PRIOR FILING DATE: 1997-02-06
PRIOR PELING DATE: 1997-02-06
PRIOR FILING DATE: 1996-03-12
PRIOR PELICATION NUMBER: US 60/013,285
PRIOR FILING DATE: 1996-03-12
PRIOR FILING DATE: 1996-03-12
PRIOR FILING DATE: 1996-03-12
PRIOR PELICATION NUMBER: US 60/013,285
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Pred. No. 8.6e-189;
1; Mismatches 5;
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Patent No. 6713061
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Best Local Similarity 97.1<sup>1</sup>
Matches 409; Conservative
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; ORGANISM: Homo sapiens
US-09-557-908-2
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TSTLGSCPERCAAVGGWRQMFWQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240
                                                                                                                                                                                                                                                301 DQLPSRALGPAAAPTLSPESPAGSPAWILQPGPQLYDVWDAVPARRWKEFVRTLGLREAE 360
                                                     181 TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240
                                                                                                                                          DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
                                                                                                           MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
                                                                                                                                                                                                                                                                                                                             361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Gentz, Reiner L.
TILE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
CLASSIPICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DAMA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MRR-1996
ATTONEY/AGERI INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1488.0310003/EKS/KRM
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Patent No. 6153402
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REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14(
TELECOMMUNICATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
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Matches 409; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dii
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MinPatin (Genentech)
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/928,069
FILING DATE: 11-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08928069;
Patent No. 6462176;
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15;
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Genentech, Inc.
           36,688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 97.1'
Matches 409; Conservative
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        REGISTRATION NUMBER:
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US-08-928-069-1
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                                                                                     LKAPCTEPCGNSTCLVCPQDTFLAWENHINSECARCQACDEQASQVALENCSAVADTRCG 116
                                                                                                                                  68 LKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCG 127
                                                                                                                                                                                                                                                                                                                      236
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                                                                                                                                                                                                   117 CKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGC 176
                                                                                                                                                                                                                                                              187
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                                                                                                                                                                                                                                               128 CKPGWFVBCQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGC
237 DEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQV
                                                                                                                                                                                                                                                                                                                   177 VSCPTSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C. STREET: 1100 New York Ave., NW, Suite 600 CITY: Washington
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
Dixit, Vishava
APPLICANT:
APPLICA
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTITE: BEATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/33,966
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
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APPLICATION NUMBER: No. 6759513 Yet Assigned
FILING DATE: 06-FEB-1997
BRICH APPLICATION DATA: 06-FEB-1997
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-CT-1996
PRIOR APPLICATION DATA: US 60/013,285
APPLICATION NUMBER: US 60/013,285
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09333966
Patent No. 6759513
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 CKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 VSCPISTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 DEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 REAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRG 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TWSWDQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGL 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                           LKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 REAEIEAVEVEIGRFRDQOYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRG
                                                                                                                                                                                                                                                                                                                                                                                                            3 QRPRG-----CAAVAAALILUVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 VSCPTSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                              Length 428;
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REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMINICATION INFORMATION:
TELEBRAX: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: 11near
                                                                                                                                                                                                                                                                                                      97.6%; Score 2267; DB 4;
97.1%; Pred. No. 8.6e-189;
tive 1; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                Query Match 45.2%; Score 1051; DB 4; Length 181; Best Local Similarity 100.0%; Pred. No. 1.3e-83; Matches 181; Conservative 0; Mismatches 0; Indels (
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/026943
FILING DATE: 09/23/1996
TOTORNEY/AGENT INFORMATION:
NAME: MAISCHAIG, DAIDE L.
REGISTRATION NUMBER: 35,600
REPERBUCE/DOCKET NUMBER: 91,600
TELECOMMUNICATION INFORMATION:
TELEPRAN: 650/225-5416
TELEFRAN: 650/225-5416
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids:
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-928-069-1
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June 27, 2005, 13:37:13; Search time 19 Seconds (without alignments)
2111.705 Million cell updates/sec Run on:

US-10-081-280-6

1 MEQRPRGCAAVAAALLLVLL......ERMGLDGCVEDLRSRLQRGP 417 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES h DB ID Description	2 JC4302 tumor necrosis	1 GQMST1 tumor necrosis		1 GQHUT1 tumor necrosis	2 A40036	2 A46484	2 JC2395	2 I37383	2 I54182	7	2 D36858	2 T28623	1 A26431 nerve growth	2 T13954 MEGF6 protein	1 GOHUN nerve	2 D72175	2 I48700	2 JC7705	1 A48225	2 S18252 heparan	2 F87908	2 T23064 hypothetical	2 T43291 laminin alpha	1 MMRTS		2 A60771	2 A48579	
Length D	 461	454	461	455	335	327	324	314	435	1548	349	348	425	1574	427	349	272	651	915	3707	2823	2823	3102	1801	2531	277	667	
% Ouery Match L	17.9	17.4	17.0	16.1	9.8	8.4	7.5	7.2	7.1	7.0	7.0	6.9	6.9	6.8	6.7	6.7	9.9	9.9	9.9	6.4	6.4	6.4	6.4	6.3	6.3	6.3	6.3	
Score	 415	404.5	394.5	374	199.5	196	175	168	166	163.5	162.5	159.5	158	158	155.5	154.5	153.5	153.5	153.5	149.5	148	148	148	147.5	146.5	146	146	
Result No.	 7	8	e	4	ហ	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	

T2 protein - myxom	furin (EC 3.4.21.7	probable proprotei	perlecan precursor	hypothetical prote	Delta-4 protein -	furin (EC 3.4.21.7	OX40 antigen precu	B cell-associated	laminin gamma-1 ch	laminin gamma-1 ch	uromodulin precurs	laminin beta-2 cha	CD27 antigen precu	hypothetical prote	laminin alpha-1 ch
GQVZML	A43434	B48225	A38096	T28811	JC7569	T43251	S12783	A46476	MMMSB2	MMHUB2	S52111	S53869	A46517	T27684	S18253
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326	1680	915	4391	1557	989	1299	271	305	1607 1	1609	642 1	1798 2	260 1	2219 2	3712
6.2 326				6.1 1557											
144.5 6.2 326		5 6.2	5 6.2	6.1	5 6.1						5.9	5.9		5.9	5.9

ALIGNMENTS

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AjGene: Infr

CjSuperfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homology

CjSuperfamily: tumor necrosis factor receptor; transmembrane protein; tumor

Fj1-29/Domain: signal sequence #status predicted <SIG, status predicted <MAT>

Fj30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>

Fj44-194/Domain: NGF receptor repeat homology <NGI>

Fj44-126/Domain: NGF receptor repeat homology <NGI>

Fj211-231/Domain: transmembrane #status predicted <TWM>

Fj211-231/Domain: signal transduction #status predicted <SIT>

Fj54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                    A;Gross-references: UNIPROT:P50555; GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g114175
A;Accession: PC4093
                                                tumor necrosis factor receptor p55 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4302; PC4093
R;Suter, B.; Pauli, U.
Gene 163, 263-266, 1995
A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 GPGLDTDCRECDNGTFTASEN-HLTQCLSCSKCRSEMSQVEISPCTVDRDTVCGCRKN-- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 EPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 STLGSCPERCAAVCGWRQMF-----WVQVLLAGLVVPLLLGATLTYTYRHCWPH--- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------KPLVTADEAGMEALTPPPATHLSPLD--SAHTLLAPPDSSEKICTV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 VECQVSQCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 VAAALLLVLLGARAQG----GTRSPR---CDCAGDFHKKIGLFCCRGCPAGHYLKAPCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 VLRALLVDVYPAGVHGLVLHPGDREKRESLCPQGKYSHPQNRSICCTKCHKGTYLHNDCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.9%; Score 415; DB 2; Length 461
30.5%; Pred. No. 1.5e-20;
Live 44; Mismatches 201; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: protein
A,Residues: 1-7 <802>
A,Experimental gource: kidney cell line 15
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 30.5%
Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-461 <SUT>
                                                                                                                                                                                                                                                                                           A; Accession: JC4302
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RESULT 1
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Unior necrosis factor receptor 1 precursor - rat
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: B36555
R;Himmler, A; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; C
B/Title: Molecular cloning and expression of human and rat tumor necrosis factor recepton
A;Reference number: A36555, MUID:91090841; PMID:1702293
                                                                                                                 A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C;Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane proteir
F;1-29/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT: P22934; GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362 C;Comment: This protein is one of two known receptors for both TNR-alpha (cachectin) and C;Superfamily: tumor necrosis factor receptor type 1 (TNRR1); NGF receptor repeat homolog C;Keywords: duplication; glycoprotein; receptor; transmembrane protein F:1-29/Domain: signal sequence #status predicted <SIG>
        Comment: This protein is one of two distantly related receptors for both TNF-alpha (cac
                                                                                                                                                                                                                                                                   F;30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F;30-212/Domain: extracellular #status predicted <EXT>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;44-82/Domain: NGF receptor repeat homology <NG3>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;160-204/Domain: NGF receptor repeat homology <NG3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 PCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 DCPSPGRDIVCRECEKGIFTASQNYLR-QCLSCKTCRKEMSQVEISPCQADKDIVCGCK- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 GWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ENQFQRYLSETHFQCVDCSPC--FNGTVTIPCKETQNTVCNCHAGFFLRESECVPC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SHCKKNEECMKLCLPPPLANVTNPODSGTAVLLPLVILLGLCLLSFIFISLMCRY 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 RHCWP-----HKPLVTADEAGMEALTPPPATHLSPLDSAHTLL-----APPDSSEK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              345 SAHPQRPDNADLAI-----LYAVVDGVPPARWKEFWRFWGLSEHEIERLEMQNGRCLRE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 PISTLGSCP--ERCAAVC------GWRQMFWVQVLLAGLVVPLLLGATLTYTY 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 PKWRPEVYSIICRDPVPVKEEKAGKPLTPAPSPAFSPTSGFNPTLGFSTPGFSSPVSSTP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 ICTVQLVGNSW-----TPGY-PETQEALC----PQVTWSWDQLPSRALGPAAAP 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 ISPI-FGPSNWHFMPPVSEVVPTQGADPLLYESLCSVPAPTSVQKWED------ 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRD 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;213-235/Domain: transmembrane #status predicted <MEM>
F;236-454/Domain: intracellular #status predicted <INT>
F;54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 VAAALLLVLLGARAQGGT------RSPRCDCAGDFHKKIGLFCCRGCPAGHYLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQYEMLKRWRQQQPA---GLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

17.4%; Score 404.5; DB 1; Length
Best Local Similarity 27.2%; Pred. No. 7.5e-20;
Matches 127; Conservative 56; Mismatches 191; Indels
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A; Residues: 1-461 < HIM>
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                                                C;Genetics:
A;Gene: TNFR-2
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R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
Wol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
A;Reference number: A40254; WUID:91246168; PMID:1645445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-644 <GQ2>
A; Cross-reterences: 1-649 + GQ2>
A; Cross-reterences: 1-649 + GD2>
B; Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis, A.M.; Gray, P.W.; Feldma
Eur. J. Immunol. 21, 1649-1656, 1991
Eur. J. Immunol. 21, 1649-1656, 1991
A; Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis
A; Reference number: $16677; MUID:91285014; PMID:1647956
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R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
Mol. Immunol. 30, 165-176, 1993
A;Title: Genomic organization and promoter function of the murine tumor necrosis factor A;Reference number: 157826; MUID:93156721; PMID:8381516
A;Accession: 157826
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NiAlternate names: tumor necrosis factor receptor, 55K
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
C;Accession: A38634; B40254; Si6677; S19021; I54532; I57826
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E Proc. Natl. Acad Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of CDNAs for two distinct murine tumor necrosis factor A;Reference number: A38634; WUID:91187885; PMID:1849278
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                                                                                                                                                                                                                                                                                                                        353 APAQLADADPATLYAVVDGVPPTRWKEFVRRLGLSEHEIERLELONGRCLREAOXSMLAE 412
245 IICGKSTPVKEGEPEPLATAPSFG-----PITTFSPIPSFSPTTFSPVPSFSPISSP 297
                                                                                                                         --ESPAG 323
                                                                                                                                                                                                  298 TFTPCDWSNIKVTSPPKEIAPPPQGAG----PILPMPPASTPVPTPLPKWGGSAHSAHS 352
                                                                                                                                                                                                                                                                           SPAMMLOPGP-QLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDOQYEMLKR 381
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A; Residues: 1-454 cARR>

A; Cross-references: ENBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579

R; Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.

R; Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.

R; Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.

A; Rotelics A; 338-340, 1991

A; Ritle: Molecular cloning and expression of the mouse Inf receptor type

A; Reference number: S19021; MUID:92039815; PMID:1657766
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A;Residues: 1-454 <ROT>
A;Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
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A,Cross-references: GB:M76656; NID:g202100; PIDN:AAA40465.1; PID:g202102
                                                                                                                     QLVGNSWT----PGYPETQEALCPQVTWSWDQLPSRALGPAAAPTLSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                     382 WRQ---QQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumor necrosis factor receptor 1 precursor - mouse
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A; Residues: 1-454 < LEW>
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A; Residues: 1-454 <RES>
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A; Note: part of this sequence, including the amino end of the mature protein, confirmed P; Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.; Call f., 361-370, 1990
A; Title: Molecular cloning and expression of a receptor for human tumor necrosis factor. A; Reference number: A34900; MUID:90235285; PMID:2158863
A; Accession: A34900
A; Molecule type: mRNA
A; Residues: 1-455 < SCH>
A; Residues: 1-455 < SCH>
A; Residues: 1-455 < SCH>
A; Cross-references: GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
B; Himmler, A.; Maurer-Pogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; CAPA, Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor A; Reference number: A36555; MUID:91090841; PMID:1702293

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18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 N----QPQRYLSETHFOCVDCSPC--FNGTVTTPCKEKQNTVCNCHAGFFLSGNECTPC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 AGSPAMMLQPGP-QLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVGGR-FRDQQYEML 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 PTSTLGSCP--ERCAAVC-----GWRQMFWVQVLLAGLVVPLLLGATLTYTYR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 ----SHCKKNQECMKLCLPPVANVTNPQDSGTAVLLPLVIFLGLCLLFFICISLLCRYP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 H------CWPHKPLVTADEAGM--EALTPPPATHLSPLDSAHTLL-----APPD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 OWRPRVYSIICRDSAPVKEVEGEGIVTKPLTPASIPAFSPNPGFNPTLGFSTTPRFSHPV 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 SSTPISPV-FGPSNWHNFVPPVREVV---PTQGADPLLYGSLNPVPIP--APVRKWEDVV 351
                                                                                                                                                                                                                                                                                                                                                                             11 VAAALLLVILGARAQG-----GTRSPR---CDCAGDFHKKIGLFCCRGCPAGHYLKA 59
                                                                                                                                                                                                                                                                                                                                                                                                                        11 LSLVLLALLMGIHPSGVTGLVPSLGDREKRDNLCPQGKYAHPKNNSICCTKCHKGTYLVS 70
F;30-461/Product: tumor necrosis factor receptor type 1 #status predicted < F;30-211/Domain: extracellular #status predicted < EXT>
F;30-211/Product: tumor necrosis factor binding protein #status predicted < F;410-211/Product: tumor necrosis factor binding protein #status predicted < F;44-212/Domain: NGF receptor repeat homology <NG1>
F;44-212/Domain: NGF receptor repeat homology <NG3>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;212-234/Domain: Transmembrane #status predicted < MEM>
F;212-234/Domain: intracellular #status predicted < INT>
F;54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                            73;
                                                                                                                                                                                                                                                                         ; Score 394.5; DB 1; Length
; Pred. No. 3.6e-19;
55; Mismatches 202; Indels
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Best Local Similarity 27.9*
Matches 128; Conservative
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A Molecule type: protein
A; Molecule type: protein
A; Molecule type: 30-36; A. (55-79, 'XX', 82-94, 'NK'; XX', 100-104;107-128;162-167, 'X', 169-2(
A; Note: the purified protein, called tumor necrosis factor binding protein, is a soluble
B; Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. (Natl. Acad. S21. U.S. A. 87, 7380-7384, 1990
A; Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of rec
A; Reference number: A38281; MUID:91017509; PMID:2170974

A,Molecule type: mRNA A,Residues: 1-452 - AHIM> A,Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756 A,Accession: C36555

A;Accession: A36555

A; Molecule type: mRNA A; Residues: 1-455 <GRA> A; Cross-references: GB:M37764 A; Note: Ash authors translated the codon TGG for residue 371 as Thr, AAG for residue 372 A; Note: Y: Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann, EMBO J. 9, 3269-3278, 1990 A; Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The CDNA for the type

A; Accession: A38281

le form of the receptor. A;Reference number: \$12057; MUID:91006021; PMID:1698610 A;Accession: \$12057

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A; Molecule type: mRNA
A; Residues: 1-455 < NOP>
A; Residues: 1-455 < NOP>
A; Residues: 1-455 < NOP>
A; Cross-references: BMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
A; Cross-references: BMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
A; Cross-references: Dates of soluble TNF binding protein 1, including its amino and carboxyl ends, R; Kemper, O.; Wallach, D.
Gene 134, 209-216, 1993
A; Title: Cloning and partial characterization of the promoter for the human p55 tumor shaference number: JT0758; WUID:94085779; PMID:8262379
A; Reference number: JT0758; WUID:94085779; PMID:8262379

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Unior necrosis factor receptor 1 precursor [validated] - human
N.Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1
N.Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein (S.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
A.Speciesion: Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, P.F.
Genomics 13, 219-224, 1992
A.;Title: Structure of the human TNF receptor 1 (p60) gene (TNRF1) and localization to change facession: A38208, MUID:92250049; PMID:131577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-452 s-FUC.
A; Residues: 1-452 s-FUC.
A; Residues: 1-452 s-FUC.
A; Cross-references: UNIPROT: P19438; GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:A
A; Cross-references: UNIPROT: P19438; GB:M75864; R:; Brockhaus; M:; Tabuchi, H:; Lesslau
Cell 61, 351-359, 1990
A; Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor receptance number: A34899; MUID:90235284; PMID:2158862
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A; Molecule type: mRNA A; Residues: 1-455 <LOE> Accession: A34899

A; Molecule type: protein
A; Residues: 41-60 <GAT>
A; Experimental source: cancer patient serum
R; Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
Bur. J. Haematol. 42, 270-275, 1989
A; Title: Isolation and characterization of a tumor necrosis factor binding protein from vareference number: A60594; MUID:89171156; PMID:2924890
A; Reference number: A60594
A; Molecule type: protein
A; Residues: 41-43, X', 45-53, V', 55-57, XX', 60 <OLS>
A; Residues: 41-43, X', 45-53, V', 55-57, XX', 60 <OLS>
A; Experimental source: renal failure patient urine
B; Experimental source: renal failure patient urine
B; Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990 A;Cross-references: GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754 A;Experimental source: placenta

Riseckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.

Eur. J. Immunol. 20, 1167-1174, 1990
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequence
A;Reference number: A60231; MUID:90292116; PMID:2113477
A;Recession: A60231

A, Residues: 1-13 < KEM> A; Molecule type: DNA

A;Molecule type: protein A;Residues: 41-43,'X',45-53,'X',55-57 <SEC> R;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Ler Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990 A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto)

A;Reference number: A38258; MUID:91062364; PMID:2174164 A;Accession: A38258

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A; Accession: A40036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Across-references: GDB:125913; OMIM:191190
A; Map position: 12p13.2-12p13.2
C; Superfamily: tumor necrosis factor receptor type 1 (TNRI); NGF receptor repeat homology c; Keywords: duplication; glycoprotein; receptor; transmembrane protein
C; Keywords: duplication; glycoprotein; receptor; transmembrane protein
C; Keywords: duplication; glycoprotein; receptor; transmembrane protein
C; Keywords: duplication; glycoprotein; receptor; receptor; factor alpha inhibitor)
E; 71-21/Domain: extracellular #status predicted < RAT>
E; 74-22/Domain: NGF receptor repeat homology < NG3>
E; 74-22/Domain: NGF receptor repeat homology < NG3>
E; 71-167/Domain: NGF receptor repeat homology < NG3>
E; 71-167/Domain: NGF receptor repeat homology < NG3>
E; 71-234/Domain: nGF receptor repeat homology < NG3>
E; 71-254-145, 151/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
A;Reference number: A35010; MUID:90110215; PMID:2153136
A,Accession: A35010
                                                                                                                                                                                                                                 R;Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechinol. Blochem. S9, 2266, 2266, 1994
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified A;Reference number: JC2404; MUID:95128033; PMID:7765720
                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
A;Experimental source: urine
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AAAPTLSP- 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 EC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 TSTLGSCPE--RCAAVC------GWRQMFWVQVLLAGLVVPLLLGATLTYTYRH 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---SNCKKSLECTKLCLPQIENVKGTEDSGTTVLLPLVIFFGLCLLSLLFIGLMYRYQR 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 CWPHK-----PLVTADEAGMEALTPPPATHLSPLDS-----AHTLLAPPDSSEKIC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -WKSKLYSIVCGKSTPEKEGELEGTTTKP---LAPNPSFSPTPGFTPTLGFSPVPSSTFT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ESPAGSPAMMIQPGP-QLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRD 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLLVLLGARAQG------GTRSPR---CDCAGDFHKKIGLFCCRGCPAGHYLKAPCTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.1%; Score 374; DB 1; Length 455; Best Local Similarity 28.3%; Pred. No. 8.2e-18; Matches 131; Conservative 49; Mismatches 183; Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 TVQLVGNSWTPGYPETQEALCPQVTWSWDQLPSRALGP--
                                                                                                                                                                                                    A; Experimental source: normal urine
                                                                                                                                           A; Molecule type: protein A; Residues: 41-45 < ENG>
                                                                                                                                                                                                                                                                                                                                                            A; Accession: JC2404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene: GDB:TNFR1
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Ajaccession: S24543
Ajstatus: preliminary
Ajmolecule type: mRNA
Ajmolecule type: mNJD:92268122; PMID:1375228
Ajmolecule type: mmmber: Aj8142; MUID:92268122; PMID:1375228
apoptosis-mediating surface antigen Fas precursor - human NyAlternate names: surface antigen APO-1 C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 17-Jan-1992 #sequence revision 17-Jan-1992 #text_change 09-Jul-2004 C;Accession: A40036; S24543; Ā38142 R;Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Hase, Cell 66, 233-243, 1991 A;File: The polypeptide encoded by the cDNA for human cell surface antigen Fas can media A;Reference number: A40036; MUID:91309137; PMID:1713127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Map position: 10g24.1-10g24.1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C;Keywords: apoptosis; surface antigen; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;85-128/Domain: NGF receptor repeat homology <NG4*
F;174-190/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P25445; GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410
R;Krammer, P.H.
submitted to the EMBL Data Library, February 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 LENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 TCLPGFYEHGDGCVSCPTSTLGSCPERCAAVCGWR-QMFWVQVLLAGLVVPLLLGATLTY 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----EHGI-IKECTLTSNTKCKEE-----GSRSNLGWLCLLL--LPIPLIVWVKRKE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 TYRHCWPHKPLVTADEAGMEALTPPPATHLSPLDSAHTL---LAPPDSSEKICTVQLVGN 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWTPGYPETQEALCPQVTWSWDQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVM 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 VOKTCRKHR----KENOG-----SHESPTLNPETVAINLSDVDLSKYITTI----
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21.4%; Pred. No. 2.8e-06;
tive 43; Mismatches 106; Indels 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Kacus: preliminary; not compared with conceptual translation A; Molecule type: nucleic acid A; Residues: 1-134, 'Q', 136-335 < OEH>
A; Residues: 1-134, 'Q', 136-335 < OEH>
A; Experimental source: SKW6.4 cells A; Note: sequence extracted from NCBI backbone (NCBIP:103810) A; Note: in NCBI backbone the source is designated as mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---AGVMTLS-
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A;Cross-references: GDB:132671; OMIM:134637
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Matches 74; Conserva
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A;Molecule type: mRNA
A;Residues: 1-335 <ITO>
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RESULT

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A; Molecule type: mRNA
A; Residues: 1-62, 'RFT' <KI2>
A; Cross-references: DBJ:D26113; NID:g468488; PIDN:BAA05109.1; PID:d1005651; PID:g468489
A; Experimental source: liver
C; Genetics:
A; Introns: 62/1
C; Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog C; Keywords: transmembrane protein
F; 1-21/Domain: signal sequence #status predicted <SIG>F; 2-334/Product: Fas antigen #status predicted <MAT>F; 4-79/Domain: NGF receptor repeat homology <NGF>F; 81-124/Domain: Transmembrane #status predicted <TWM>
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C;Date: 02-Uul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 137383
R;Cascino, I.; Flucci, G; Papoff, G.; Ruberti, G.
J. Immunol. 154, 2706-2713, 1995
A;Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule A;Reference number: 137383; MUID:95181785; PMID:7533181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 TCLPGFYEHGDGCVSCPTSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 ERKVKDCTTSGGAPTCHPCTEGEEYTDRKHYSDKCRRCAFCDEGHGLEVETNCTRTQNTK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 GLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 WIPGYPETQEALCPQVTWSWDQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMD 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 YRHCWPHKPLVTADEAGMEALTPPPATHLSPLDSAHTL---LAPPDSSEKICTVQLVGNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----GIRSPRCDCAGDFHKKIGLFCCRGCPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.2%; Score 16%; DB 2; Length 314;
19.1%; Pred. No. 0.00034;
tive 37; Mismatches 100; Indels 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 EINCTRIQNTKCRCKPNFF-----CNSTVCEHCDPCTKC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 AVPARRWKEFVRTLGLREAEIEAVEVE-IGRFRDQQYEMLKRWRQ 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 7.5%; Score 175; DB 2; Local Similarity 28.5%; Pred. No. 0.00012; Ne 43; Conservative 17; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AGVMTLS-
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A;Molecule type: mRNA
A;Residues: 1-314 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCKPGWFVECQVSQCVSSSPFYCQPCLDCG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 ----EHGI-IKECTLTSNTKCKEE----
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Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137383
FAS soluble protein - human
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Best Local Si
Matches 43,
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                                     apoptosis-mediating membrane-associated polypeptide Fas - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 .
C:Accession: A46484; A47254
R:Matanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkins, J. Immunol. 148, 1274-1129, 1992
A:Timunol. 148, 1274-1129, 1992
A:Title: The CDNA structure, expression, and chromosomal assignment of the mouse Fas ant A;Reference number: A46484; MUID:92148151; PMID:1371136
                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-37 < MAT:
A; Cross-references: UNIPROT: P25446; GB: M83649; NID: g193225; PIDN: AAA37593.1; PID: g193226
A; Experimental source: BAM3 macrophage cell line
A; Note: sequence extracted from NCBI backbone (NCBIN: 81544, NCBIP: 81545).
R; Adachi, M.; Wattanabbe-Fukunaga, R.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 193
A; Title: Aberrant transcription caused by the insertion of an early transposable element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: JC2395
A;Molecule type: mRNA
A;Residues: 1-34 <KIM>
A;Cross-references: UNIPROT:Q63199; DDBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:d1005
A;Experimental source: thymus
A;Accession: PC2246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506
A;Experimental source: MRL lpr/lpr
A;Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:126863, C;Superfamaily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo C;Keywords: transmembrane protein
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NGF>
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: 70:295; FC2246
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A;Title: A variant mRNA species encoding a truncated from of Fas antigen in the A;Reference number: JC2395; MUID:94128114; PMID:7507668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AVLPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQG-GPFCCQPGKK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- DCAGDFHKKIGLFCCRGCPAGHY
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8.4%; Score 196; DB 2; Length 327;
Best Local Similarity 23.8%; Pred. No. 4.7e-06;
Matches 62; Conservative 25; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 AALLLVLLGARAQGGTRSPRC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Status: preliminary
A,Molecule type: nucleic acid
A,Residues: 1-96 <ADA>
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C; Keywords: hydrolase; serine proteinase
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A;Accession: D36858
A;Status: preliminary
A;Molecule type: DNA
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A; Residues: 31-168 <SHC>
                                                                      Local Similarity
nes 82; Conserv
                                                                                                                                                                                                                           81 WENHINSEC-
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A,Status: preliminary
A,Molecule type: DNA
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                                                 Query Match
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R;Baens, M;; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
A;Reference number: 154182; MUID:93252381; PMID:8486360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Map position: 12p13.3-12p13.1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homold
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A/Cross-references: UNIPROT:Q04592; GB:D17583; NID:g407344; PIDN:BAA04507.1; PID:d100503
                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P36941; GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
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R;Nakagawa, T.; Murakami, K.; Nakayama, K.
R;Nakagawa, T.; Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 6
A;Title: identification of an isoform with an extremely large Cys-rich region of A;Reference number: S34583; MUID:93327934; PMID:8335106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 --COPHTRCENOGLVEAAPGTAQSDTTCKNPLEPLPPEMSGT------MLMLAVLL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 PLLLGATLTYTYRHCWPHKPLVTADEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKIC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 PLAFFLLLATVFSCIWKSHPSL-CRKLGSLLKRRPQGEGPNP---------273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 TVQLVGNSWTP--GYPETQEALCPQVTWSWDQLPSRALGPAAAPTLSPESPAGSPAMMLQ 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 ----VAGSWEPPKAHPYFPDLVQPLLPISGDVSPV-STGLPAAPVLEAGVPQQQSPLDLT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 LLLVLLGARAQG-----GTRSPRC-DCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumor necrosis factor receptor 2-related protein - human
C,Species: Homo sapiens (man)
C,Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     serine proteinase (EC 3.4.21.-) PC6B - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.1%; Score 166; DB 2; Length 435; Best Local Similarity 21.1%; Pred. No. 0.00063; Matches 77; Conservative 43; Mismatches 153; Indels
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GDB:1230195; OMIM:600979
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A;Molecule type: mRNA
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A;Cross-references: UNIPROT:P34015; GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A;Experimental source: strain India-1967, ssp. major, isolate Ind3
R;Kolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolc submitted to the EMBL Data Library, April 1992
A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P (
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A;Experimental source: strain India-1967, isolate Ind3
A;Exbelshunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A;Reference number: S32385; MUID:93202281; PMID:8384129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology F;32-6/Domain: NGF receptor repeat homology <NGF-F;68-109/Domain: NGF receptor repeat homology <NGF-F;68-109/Domain: NGF receptor repeat homology <NGF-F;110-151/Domain: NGF-F;110-151/Domain: NGF-F;110-151/Doma
                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       616 OGSGPSNCTSCRADKHGOERFLYHGECLENCPVGHY-----PAKGHTCLPCPDNCELC 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- ARCQACDEQASQVALENCSAVADTRCGC--- KPGWF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VECOVS-----QCVSSSP-----FYCQPC-LDCGALHRHTRLLCSRRDTDCGTCLPG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              727 TSCATGYYMFERHCYKACPEKTFGVKWECRACGINCGSCDQH------ECYWCEEG 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FYEHGDGCV-SC----PISTLGSCPERCAAVC-----GWRQMFWVQVLLAGLVVPLLL 216
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N/Alternate names: B2R protein (COP)
C/Species: variola virus
C/Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: D36858; S46888; S32385; S35987
                                                                                                                                                                                                                                                                                                                        25 QGGTRSPRCDCAGDFHKKIGLF----CCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLA
Length 1548;
        DB 2;
7.0%; Score 163.5; DB 2; ilarity 24.5%; Pred. No. 0.0031; Conservative 22; Mismatches 138;
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A;Experimental source: strain India-1967, ssp. major
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A;Cross-references: GRIS61269
A;Cross-references: GRIS61269
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cs C;Comment: This protein is found on sensory and sympathetic neurons, on neuroblastomary c;Comment: This protein is thought to form a high-affinity receptor when it associates wing C;Comment: This protein is thought to form a high-affinity receptor when it associates wing C;Comment: This protein is thought to form a high-affinity receptor when it associates wing C;Genetics:
A;Infrons: 20/3
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology c;Reywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; F;30-425/Product: nerve growth factor receptor #Extra predicted cMAT>
F;30-251/Domain: NGF receptor repeat homology cMG3>
F;30-551/Domain: NGF receptor repeat homology cMG3>
F;110-148/Domain: NGF receptor repeat homology cMG3>
F;150-190/Domain: NGF receptor repeat homology cMG3>
F;150-190/Domain: NGF receptor repeat homology cMG3>
F;150-190/Domain: intracellular #status predicted cMEM>
F;252-273/Domain: intracellular #status predicted cINT>
F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted
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MESFG protein - rat
C.Species: Rattus norvegicus (Norway rat)
C.Species: Rattus norvegicus (Norway rat)
C.Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C.Accession: T13954
R.Maxayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
R.Maxyama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
R.Maxyama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
R.Matile: Identification of high-molecular-weight proteins with multiple EGF-like motifs handcession: T13954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 AVCRCAYGYYQDEETGHCEACSVCEVGSGLVFSCQ------DKQNTVCEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.8%; Score 158; DB 1; Length 425;
21.2%; Pred. No. 0.0021;
Ive 42; Mismatches 202; Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  llarity 21.2%;
Conservative 4
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Matches 102; Conserve
            A; Residues: 1-20 <MET>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Mesidues: 1-425 cRAD:
A; Cross-references: UNIPROT: P07174; GB: X05137; NID: 956755; PIDN: CAA28783.1; PID: 956756
R; Metsis, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
R6met 21, 247-254, 1992
A; Title: Regulatory elements and transcriptional regulation by testosterone and retinoic
A; Reference number: PH1229; MUID: 93077038; PMID: 1446821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: UNIPROT:P34015; EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g4391
A,Experimental source: strain Bangladesh 1975
C,Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor. A;Reference number: A26431; MUID:87115859; PMID:3027580
                                                                                                                                                                                                                                                                                                                                     QDTFLAWENHHNSECARCQA-CDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSS 133
                                                                                                                                                                                                                                                                                                                                                                                    70 SGTFTS-RNNHLPACLSCNGRCN--SNQVETRSCNTTHNRICECSPGYY-----CLLK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 GSSGCKACVSQTKCGIGYGVSGHT---SVGDVICSPCGFGTYSHTVSSADKCEPVPNNT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 GTFTS-RNNHLPACLSCNGRCN--SNQVETRSCNTTHNRICECSPGYY------CLLKG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 SPFYCQPCLD---CG---ALHRHTRLLCSRRDTDCGTCLPGFYEH----GDGCVSCPTST 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DTFLAWENHHNSECARCQA-CDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSS 134
                                                                                                                                                                                                                                  LSCIIINGRDAAPYTPPNGKCKDTEYKRHNL-CCLSCPPGTYASRLCDSKT-NTQCTPCG 69
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NiAlternate names: NGF receptor
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A26431; PH1229
R;Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQ
                                                                                                                                                                       LLLVLLGARAQGGTRSPRCDCAGDFHXKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
7.0%; Score 162.5; DB 2; Length 349; 26.7%; Pred. No. 0.00087; tive 21; Mismatches 84; Indels 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.9%; Score 159.5; DB 2; Length 348; 26.8%; Pred. No. 0.0014; Indels 27.
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Molecule type: DNA
                                                                                     Conservative
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A; Molecule type: DNA
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A;Gene: GDB:NGFR
A;Cross-references: GDB:120234; OMIM:162010
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Job time : 21 secs
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                             A;Residues: 1-1574 «NAK»
A;Cross-references: UNIPROT:O88281; EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3
A;Expeximental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF6
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A; Residues: 1-427 < JOHN
A; Residues: 1-427 < JOHN
A; Residues: 1-427 < JOHN
A; Cross-references: UNIPROT: P08138; GB: M14764; NID: g189204; PIDN: AABS9544.1; PID: g189205
A; A; Ararano, N.; Dietzschold, B.; Earley Jr., J.J.; Schatteman, G.; Thompson, S.; Grob, P.;
J. Neurochem. 48, 225-232, 1987
A; Title: Purification and amino terminal sequencing of human melanoma nerve growth factors.
A; Reference number: A60204; MJID: 87085574; PMID: 3025363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1089 COLNCSCLHGGICDRLTGHCLCPAGWTGDKCOSSCVSGTFGVHCEEHCACRKGASCHHVT 1148
                                                                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                                                                                                            990 CAQSCPPLTF-----GLNCSQICTCPNGAS-----CDSVTG-QCHCAPGWMGPTCLQ 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1036 ACPPGLYGKNCOHS-CLCRNGGRCDPILGOCTCPEGWTGLACENE-----CLPGHYAAG 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1149 GACPCPPGWRGPHCEQACPRGWFGEACAQRCLCPINASC--HH--VTG-----ECRCPPG 1199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1200 FTGL------SCEQAC-----SCEQAC------0PGTFGKDCEHLCQCPGETWACD--PA 1234
                                                                                                                                                                                                                                                                                                                                                   73 ----CPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWF----- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                       -----VECQVSQCVSSSPFYCQPCL-DCGALHRHTRLLCSRRDTDCGTCLPGFYE-- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAGMEALTPPP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 ATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPG-YPETQEAL--CPQVTWSWDQLPS 305
                                                                                                                                                                                                                                                                                                        333 ŚGACTCPAGWR---GSFCEHACPAGFFGLDCDSACNCSAGAPCDAVTGSCICPAGRWGPR 989
                                                                                                                                                                                                                                                               30 SPRCDCAGDFHKKIGLFCCRGCPAGHY-----LKAPCTEPCGNSTCLV----
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                          6.8%; Score 158; DB 2; Length 1574;
24.5%; Pred. No. 0.0072;
ive 16; Mismatches 120; Indels 142;
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                      Query Match
Best Local Similarity
Matches 90; Conserv
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A Map position: 17g21-17g22

C)Superfamily: nerve growth factor receptor; NGF receptor repeat homology

C)Superfamily: nerve growth factor receptor; NGF receptor repeat homology

C)Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t;

E)1-28 Domain: signal sequence #status predicted <SIG>
F)29-427/Product: nerve growth factor receptor #status experimental <MAT>
F)29-520/Domain: extracellular #status predicted <SET>
F)32-65/Domain: NGF receptor repeat homology <NG3>
F)40-148/Domain: NGF receptor repeat homology <NG3>
F)149-189/Domain: NG5/Domain: NG5/Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Cross-references: GB:M21621, NID:g189206, PIDN:AAA36363.1; PID:g189207
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma of
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of t
C;Comment: This protein is thought to form a high-affinity receptor when it associates wi
C;Comment: This receptor undergoes both N- and O-linked glycosylation.
R;Sehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A;Title. A constitutive promoter directs expression of the nerve growth factor receptor (A;Reference number: 157638; MUID:89096903; PMID:2850481
A;Accession: 157638
A;Accession: 157638
A;Accession: 157638
A;Accession: 157638
A;Residues: 1-22 <RES>
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F;273-427/Domain: intracellular #status predicted <INT>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 27, 2005, 13:37:13; Search time 176 Seconds (without alignments) 1213.279 Million cell updates/sec Run on:

US-10-081-280-6 2323 1 MEQRPRGCAAVAAALLIVLL......ERMGLDGCVEDLRSRLQRGP 417 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	* 2			SUMMAKIES	
Score	Match	Length DB	DB	ΙD	Description
2323	100.0	417	1	TR25 HUMAN	Q93038 h tumor nec
1397	60.1	413	~	Q99MM1	Q99mml mus musculu
1255	54.0	387	~	Q8VD70	Q8vd70 mus musculu
415	17.9	461	-	TRIA PIG	P50555 sus scrofa
406.5	17.5	440	7	Q6QH <u>F</u> 0	Q6qhf0 mus musculu
405.5	17.5	440	~	Q6QHF2	Q6qhf2 mus spretus
404.5	17.4	440	7	Q6QHF1	Q6qhf1 mus musculu
404.5	17.4	454	Н	TRIA MOUSE	P25118 mus musculu
394.5	17.0	461	-	TR1A_RAT	P22934 rattus norv
387.5	16.7	471	Н	TRIA_BOVIN	019131 bos taurus
374	16.1	455	Н	TR1A HUMAN	P19438 homo sapien
365	15.7	446	7	Q95N <u>D</u> 3	Q95nd3 felis silve
247.5	10.7	332	٦	TNR6 PIG	077736 sus scrofa
226	9.7	319	7	Q9TV79	Q9tv79 oryctolagus
223.5	9.6	389	~	Qenuue	
221	9.5	314	~	Q861W6	Q861w6 felis silve
217.5	9.4	320	7	Q9XS29	Q9xs29 oryctolagus
214.5	9.5	328	7	Q76B99	Q76b99 xenopus lae
211.5		328	~	Q6GLZ4	Q6glz4 xenopus lae
206.5	8.9	283	ч	TR14 HUMAN	Q92956 homo sapien
205	8.8	438	7	Q9DFV0	
203.5	8.8	368	7	057408	O57408 meleagris
'n	8.8	440	Н	T10B_HUMAN	
200.5	•	283	7	8 <u>Z</u> SX6 <u>D</u>	
200	8.6	381	Н	T10B MOUSE	
S	9.8	335	Н	TNR6 HUMAN	
S	•	368	7	Q91AR7	-
8	•	189	~	Q95185	
198		263	7	09XX6O	Q9xs60 oryctolagus
97.5	8.5	276	~	Q71F55	mus mus
'n	8.5	333	-	TNR6 MACMU	Q9bdp2 macaca mula

097530 canis famil 097491 ovis aries 097491 ovis aries 091814 mus musculu 080wm9 mus musculu 080se9 homo sapien 090400 macaca neme 090400 macaca neme 090400 macaca neme 090400 macaca neme 090400 macaca mula psile67 bos taurus 060491 xenopus tro 06uxm8 homo sapien 090m79 gallus gall
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197 196.5 196.5 195.5 193.5 193.5 191.5 191.1 191.1 191.5 189.5
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ALIGNMENTS

RESULT	1.1.
IRZS	1725_HUMAN STANDARD: PRT: 417 AA.
	000277; 00027
Q Z	Q92983; Q93036; Q93037; Q99722;
	037031; QFB100; QFUMBU; QFUMBU; 01-NOV-1997 (Rel. 35, Created)
	01-NOV-1997 (Rel. 35, Last sequence update)
i d	05-JUL-2004 (Rel. 44, Last annotation update) Theory negroes factor recentor emergemily member 25 precureor (MSI-1
3 E	lumoi neciosis incroi leceptoi supellamili member 2) preculso: (WSD-1 nrotein) (bromtosis-medisting receptor DB3) (bromtosis-medisting
3 B	receptor TRAMP) (Death domain receptor 3) (WSL protein) (Apoptosis
DE	inducing receptor AIR) (Apo-3) (Lymphocyte associated receptor of
3 6	death) (IARD) (UNQ455/PRO779).
2 c	Name=INFKSF25; Synonymb=APO3, DDK3, DK3, INFKSF12, WSL, WSL1; Homo ganjeng (Himan)
88	
8	ia; Primates; Catarrhini
ŏ	NCBI_TaxID=9606;
2 6	(L1) SECTIENCE PROM N & (TEOFORMS 1 - 3 AND 4) AND MITTAGENESTS
ű	TISSUE-Lymphoid:
2	MEDLINE=97088617; PubMed=8934525; DOI=10.1038/384372a0;
æ	Kitson J., Raven T., Jiang YP., Goeddel D.V., Giles K.M., Pun KT.,
æ	
RT	"A death-domain-containing receptor that mediates apoptosis.";
2	Nature 384:372-375(1996).
3 2	
¥ 5	SEQUENCE FROM N.A. (ISOFORM 1). TISSHE-Umbilical vein endothelial cells:
ž	MEDLINE=97081063; PubMed=8875942; DOI=10.1126/science.274.5289.990;
æ	Chinnaiyan A.M., O'Rourke K., Yu GL., Lyons R.H., Garg M.,
æ	Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;
RT	"Signal transduction by DR3, a death domain-containing receptor
RT	related to TNFR-1 and CD95.";
Z.	Science 274:990-992(1996).
3 6	LJ CECTENICE EDOM N A
Z Z	SECOND FROM M. Din W.S. Cosman D. Smith C.A. Goodwin R.G.:
Z	EMBL/GenBank/DDBJ databases.
N.	[4]
КР	SEQUENCE FROM N.A. (ISOFORM 1).
Z S	TISSUE=Heart;
ă	MEDLINE=97148200; Pubmed=8994832; DOI=10.1016/S0960-9822(02)70791-4;
æ	Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,
8	Goddard A.D., Bauer K.D., Ashkenazi A.;
RT	"Apo-3, a new member of the tumor necrosis factor receptor family,
RI	contains a death domain and activates apoptosis and Nr-Kappa-B.";
Z.	Curr. Biol. 6:1669-1676(1996).
<u>Z</u> :	[5]
ж е	SEQUENCE FROM N.A. (ISOFUKMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10).
ž 5	MEDLINE=Y/Z/ZZ/3; Fudmed=YII403y; DOI=IO.IO/3/phas.y4.y4.y4.z.io.io/
\$ \$	Screation G.K., Au AN., Olsen A.L., Cowper A.B., Jan K., McMichael A.J., Bell J.I.;

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(Potential)
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  ARG-254.

Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,

Rieder M. D., Bobertson P.D.,

Myamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,

Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;

"NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department

of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";

submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain, and Fetal lung;
MEDLINE=97205315; PubMed=9052819;
Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
Thome M., Bornand T. K., Hahne M., Schroeter M., Wilson A., French L.E.,
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PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
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-1-FUNCTION: Receptor for TNFSF12/APO3L/TWEAK. Interacts directly with the adaptor TRADD. Mediates activation of NF-kappa-B and induces apoptosis. May play a role in regulating lymphocyte homeostasis.
                                                                                                                                                            "A new death receptor 3 isoform: expression in human lymphoid cell lines and non-Hodgkin's lymphomas."; Blochem. Biophys. Res. Commun. 242:376-379(1998).
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"LARD: a new lymphoid-specific death domain containing receptor
                                                                            SEQUENCE FROM N.A. (ISOFORMS 11 AND 12).
MEDLINE-98113360; Pubmed-9446802; DOI=10.1006/bbrc.1997.7948;
Wazzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
                                                                                                                                                                                                                                                              Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto
Hayashi S., Sato M., Shiozawa K., Tsukamoto Y.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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                   regulated by alternative pre-mRNA splicing.";
Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
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01-MAR-2002 (TEMBLrel. 20,
01-MAR-2002 (TEMBLrel. 20,
01-MAR-2004 (TEMBLrel. 26,
                                                                                     Query Match
Best Local Similarity 62.9#
Matches 270; Conservative
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 PS50017;
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Name=Tnfrsf25;
                                                           SEQUENCE,
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PROSITE;
PROSITE;
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                                                                                                                                                                                                                                            121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP
                                                                                                                                                                                                                                                                                                       MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
                                                                                                                                                                 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG
                                                                                                                                                                                  WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP
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                                                                                                      1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; MusincBl_TaxID=10090;
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Owen M.J.;
"Genomic structure, expression, and chromosome mapping of the mhomologue for the WSL-1 (DR3, Apo3, TRAMP, LARD, TR3, TNFRSF12) gene.";
                                             Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21158384; PubMed=11261933; DOI=10.1007/8002510000290;
                                                                        0; Indels
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Last sequence update)
Last annotation update)
                                          100.0%; Score 2323; DB 1;
100.0%; Pred. No. 2.1e-153;
ive 0; Mismatches 0;
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GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR001489; Death.
InterPro; IPR011029; DEATH like.
InterPro; IPR006309; BGF like.
InterPro; IPR00930; Grow_fac_recept.
InterPro; IPR001368; TNFR_C6.
Pfam; PF00031; Death; 1.
Pfam; PF00031; Death; 1.
SMART; SM00005; DEATH; 1.
SMART; SM00005; DEATH; 1.
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EMBL; AF329969; AAK11256.1; -.
HSSP; P19438; 11CH.
EMBL; U94505; AAC51310.1; -. EMBL; U94506; AAC51311.1; -.
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01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2004 (TrEMBLrel. 26,
WSL-1-like protein.
                                                        Best Local Similarity 100. Matches 417; Conservative
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

METARUBERT R.D., Felingold E.A., Grouse L.H., Derged J.G.,

MA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A plachenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Brownetein M.J., Usdin T.B., Toshhyuki S., Carninci P., Parage C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,

Michards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 YEHGDGCVSCPTSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 YIRGNDCTSCPTGFSSVCPKACTAVCGWKQMFWVQVLLG---VAFLFGAILICAYCRWQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 QEALCPOVTWSWDQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285 QEVVCGQASQPWDQLPNRTLGTPLASPLSPAPAGSPAAVLQPGPQLYDVMDAVPARRWK
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                                                                                                                                                             Length 413;
                                                                                                                                                          60.1%; Score 1397; DB 2; Length 4 62.9%; Pred. No. 4.6e-89; ive 28; Mismatches 103; Indels
PS01186; EGF_2; UNRNOWN 1.
PS00652; TNFR NGFR 1; UNRNOWN 1.
PS50050; TNFR NGFR 2; 1.
7 413 AA; 44453 MW; 69F21B85D0DABABF CRC64;
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Last sequence update)
Last annotation update)
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Name=TNFRSF1A; Synonyms=TNFR1;
                                                                 SEQUENCE FROM N.A.
                                            NCBI_TaxID=9823;
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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Genes S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                            EQRPRGCAAVAAA------LLLVLLGARAQGGTRSPRCDCAGDFHKK1GLFCC
                                                                                                                                                                                                                                                                                                         64; Gaps
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01-OCT-1996 (Rel. 34, Last sequence update)
05-JUD-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor receptor superfamily member lA precursor (p60)
(TNF-R1) (TNF-R1) ($55).
                                                                                                                                                                                                                                                                                  54.0%; Score 1255; DB 2; Length 387; 57.7%; Pred. No. 3.2e-79; ive 26; Mismatches 92; Indels 64
                                                                                                   Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC017526; AAH17256.1; -.
R MGD; MGI:1934667; Tnfrsf25.
R GO; GO:0015615; C:extracellular space; TAS.
R GO; GO:0015615; C:extracellular space; TAS.
R GO; GO:0015021; C:integral to membrane; TAS.
R Pfam; PF00020; TNFR. C6; 1.
R SMART; SM00005; DaTH; 1.
R SMART; SM00005; TNFR. 2.
R PROSITE; PS50017; DEATH DOMAIN; 1.
R PROSITE; PS50017; DEATH DOMAIN; 1.
R PROSITE; PS0016; EGE 2; UNKNOWN 1.
R PROSITE; PS00529; TNFR. 2.
R PROSITE; PS00520; TNFR. NGFR 1; UNKNOWN 1.
R PROSITE; PS00520; TNFR NGFR 1; UNKNOWN 1.
                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                   SEQUENCE FROM N.A.
STRAIN-FVB/N; TISSUE-Salivary gland;
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Matches 248; Conservative
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TRIA_PIG

AC P5055;

DT 01-0CT-199

DT 01-0CT-199

DT 05-JUL-200

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Bukaryor, Merzos, Chordata, Crantata, Vertebrata; Buteleostomi; Memmilais, Buhrelais, Cetariodactyla; Suina; Suidae; Sus.

Memmilais, Bukaryos, Chordata, Cetariodactyla; Suina; Suidae; Sus.

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65 DCPSPGRDIVCRECEKGIFIASQNYLR-QCLSCKICRKEMSQVEISPCQADKDIVCGCK- 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 ICTVQLVGNSW-----TPGY-PETQEALC----PQVTWSWDQLPSRALGPAAAP 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 RHCWP-----HKPLVTADEAGMEALTPPPATHLSPLDSAHTLL-----APPDSSEK 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRD 373
                                                                                                            . IMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAHPQRPVNADLAI-----LYAVVDGVPPARWKEFWRFWGLSEHEIERLEMQNGRCLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 PCTEPCGNSTCLVCPQDTFLAWENHINSECARCQACDEQASQVALENCSAVADTRCGCKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 PISTLGSCP--ERCAAVC-----GWRQMFWVQVLLAGLVVPLLLGATLTYTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 ----SHCKKNEECMKLCLPPPLANVTNPQDSGTAVLLPLVILLGLCLLSFIFISLMCRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 PRWRPEVYSIICRDPVPVKEEKAGKPLTPAPSPAFSPTSGFNPTLGFSTPGFSSPVSSTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 VAAALLLVLLGARAQGGT------RSPRCDCAGDFHKKIGLFCCRGCPAGHYLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.5%; Score 406.5; DB 2; Length 440; llarity 27.2%; Pred. No. 3.3e-20; Conservative 56; Mismatches 191; Indels 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374 QOYEMLKRWRQQQPA---GLGAVYAALERWGLDGCVEDLRSRLQRGP 417
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les 127; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STLGSCPERCAAVCGWRQMP-----WVQVLLAGLVVPLLLGATLTYTYRHCWPH--- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPCGNSTCLVCPQDTFLAWENHINSECARCQACDEQASQVALENCSAVADTRCGCKPGWF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---QYRKYWSETLFQCLNCSLCP--NGTVQLPCLEKQDTIC-NCHSGFFLRDKECVSCVN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 CKNADČKNLCPATSETRNDFQDTGTTVLLPLVIFFGLCLAFFLFVGLACRÝQRWKPKLYS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -------KPLVTADEAGMEALTPPPATHLSPLD--SAHTLLAPPDSSEKICTV 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 IICGKSTPVKEGEPEPLATAPSFG-----PITTFSPIPSFSPTTTFSPVPSFSPISSP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLVGNSWT---PGYPETQEALCPQVTWSWDQLPSRALGPAAAPTLSP-----ESPAG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 TFTPCDWSNIKVTSPPKEIAPPPQGAG-----PILPMPPASTPVPTPLPKWGGSAHSAHS 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 VECQVSQCVSSSPFYCQPCLDCGALHRHTRLLC-SRRDTDCGTCLPGFYEHGDGCVSCPT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPAMMLQPGP-QLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKR 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 VLRALLVDVYPAGVHGLVLHPGDREKRESLCPOGKYSHPONRSICCTKCHKGTYLHNDCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 VAAALLIVILGARAQG----GTRSPR---CDCAGDFHKKIGLFCCRGCPAGHYLKAPCT
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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STRAIN=C57BL/6JICO; TISSUB=Liver;
Straelens J., Wielockx B., Puimege L., Vandenabeele A., Libert C.;
Students J., Wielockx B., Puimege L., Vandenabeele A., Libert C.;
Submitted (FEB-2004) to the BMBL/GenBank/DDBJ databases.
EMBL, AY541590; AAS48429.1; -.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005615; C:integral to membrane; TAS.
GO; GO:0005886; C:plasma membrane; TAS.
      By similarity.
Notinked (GlCNNc. ..) (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.9%; Score 415; DB 1; Length 461; 30.5%; Pred. No. 8.8e-21; tive 44; Mismatches 201; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       CD72361EC60C9D43 CRC64;
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461 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 PCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 DCPSPGRDTVCRECEKGTFTASQNYLR-QCLSCKTCRKEMSQVBISPCQADKDTVCGCK- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 GWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : | : | | | : | | | | 177 ----SHCKKNQECMKLCLPPPLANVINPQDSGTAVLLPLVILLGLCLLSFIFISLMCRY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 RH-----CWPHKPLVTADEAGMEALTPPPATHLSPLDSAHTLL-----APPDSS 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290 TPÍSPI-FGPSNWYFMPPVSEVVPTQGADPLLYESLCSVPAÞTFVQKWED------PA- 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 ----ENÒFQRHLSETHFQCVDCSPC--FNGTVTIPCKETQNTVCTCHAGFFLRESECVPC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 PISTLGSCP--ERÇAAVC-----GWRQMFWVQVLLAGLVVPLLLGATLTYTY 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 EKICTVQLVGNSW------TPGY-PETQEALC----PQVTWSWDQLPSRALGPAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 APTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-F 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 VAAALLLVLIGARAOG-----GTRSPR---CDCAGDFHKKIGLFCCRGCPAGHYLKA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97; Gaps
                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Statin=SPREI/Ei; TISSUE=Liver;

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0005515; F:protein binding; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

R GO; GO:0004872; F:receptor activity; IEA.

R GO; GO:0004872; F:receptor activity; IEA.

R InterPro; IPR000489; Death.

R InterPro; IPR001029; DEATH like.

R InterPro; IPR001029; EGF like.

R InterPro; IPR001369; TNFR_c6.

R Pfam; PF00201; TNFR_c6; 3.

SMART; SM00005; DEATH; 1.

R SMART; SM00005; DEATH; 1.

R SMART; SM00005; DEATH; 1.

R RARR; SM0005; DEATH; 1.

R RARR; SM0005; DEATH; 1.

R PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.

PROSITE; PS01186; EGF 2; UNKNOWN 1.

R PROSITE; PS01186; EGF 2; UNKNOWN 1.

R PROSITE; PS01086; TNFR_NGFR_1; 3.

R PROSITE; PS01086; TNFR_NGFR_1; 3.

R PROSITE; PS01086; TNFR_NGFR_2; 3.
Name-Infrsfla;
Mus spretus (Western wild mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 17.5%; Score 405.5; DB 2; Length 440; Best Local Similarity 28.1%; Pred. No. 3.8e-20; Matches 132; Conservative 56; Mismatches 184; Indels 97,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 AA; 48688 MW; 10E7ED7D289E0143 CRC64;
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                          셤
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440 AA

PRT;

PRELIMINARY;

Q6QHF1 JD Q6QHF1

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60 PCTEPCGNSTCLVCPQDTFLAWENHHNSECARCOACDEQASQVALENCSAVADTRCGCKP 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 ----ENÓFQRYLSETHFQCVDCSPC--FNGTVTIPCKETQNTVCNCHAGFFLRESECVPC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 RHCWP-----HKPLVTADEAGMEALTPPPATHLSPLDSAHTLL-----APPDSSEK 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 ICTVQLVGNSW------TPGY-PETQEALC----PQVTWSWDQLPSRALGPAAAP 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 ----SHCKKNEECMKLCLPPPLANVTNPQDSGTAVLLPLVILLGLCLLSFIFISLMCRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=DBA/2CrIBr; TISSUB=Liver;

STRAIN=DBA/2CrIBr; TISSUB=Liver;

STRAIN=DBA/2CrIBr; TISSUB=Liver;

SUBJ: ANS41589; AAS48428.1; ---

SUBJ: ANS41589; Coloured Coloured; TAS.

SUBJ: ANS41589; Coloured Coloured; TAS.

SUBJ: ANS41589; Coloured Coloured; TAS.

SUBJ: ANS41689; COLOURED; COL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             440 AA; 48632 MW; 580A2D2E334612A3 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
TNF receptor superfamily, member 1A (Fragment)
Name=Thirstia;
Mus musculus (Mouse)
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EMBL; P
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  292 ISPI-FGPSNWHFMPPVSEVVPTQGADPLLYESLCSVPAPTSVQKWED------338
                                        TLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRD 373
                                                                339 SAHPQRPDNADLAI-----LYAVVDGVPPARWKEFMRFWGLSEHEIERLEMQNGRCLRE 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-$2039815; PubMed-1657766; Rothe J.G., Brockhaus M.; Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.; "Molecular cloning and expression of the mouse Inf receptor type b."; Immunogenetics 34:338-340(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDIINE=9118788; PubMed=1849278; Lewis M., Lee A., Bennett G.L., Rice G.C., Wong G.H., Len E.Y., Goeddel D.W., Chen E.Y., Goeddel D.W., "Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species
                                                                                                                                                                                                                                                                                                                       ol-marilyy2 (Rel. 22, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor receptor superfamily member 1A precursor (p60)
(TWF-RL) (TWF-RL) (P55).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-93156721; Pubmed-8381516; DOI=10.1016/0161-5890(93)90088-S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-91285014; PubMed=1647956; MEDLINE-91285014; PubMed=1647956; MEDLINE-91285014; K., Taylor-Fishwick D.A., Cope A.P., Kissonerghis A.M., Gray P.W., Peldmann M., Roxwell B.M.J.; "Cloning, expression and cross-linking analysis of the murine p55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

BEDLINES-1246168; PubMed=1645445;
GOGGWAIN R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
Copeland N.G., Jenkins N.A., Smith C.A.;
"Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.";
Mol. Cell. Biol. 11:3020-3026(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.; "Genomic organization and promoter function of the murine tumor necrosis factor receptor beta gene.";
Mol. Immunol. 30:165-175(1993).
                                                                                                                                                      Bebo B.F., Linthicum D.S., "Nucleotide sequence of the TNF type I receptor from a mouse
                                                                                                                         374 QOYEMLKRWRQQQPA---GLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
                                                                                                                                                                                                                                                                                 454 AA
                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Tnfrsfla; Synonyms=Tnfr-1, Tnfr1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or necrosis factor receptor."; J. Immunol. 21:1649-1656(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94245292; PubMed=8188324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               endothelioma cell line.";
Immunogenetics 39:450-451(1994).
                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor necrosis
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                                                                                                                                                                                                                                                                               TRIA MOUSE
P25118;
                                          315
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STRAIN=C3H/He; TISSUE=Mesenchyme;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Liscull S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Liscull S.E., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatcheron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahesley M., Helton E., Ketteman M., Madan A., Rouffard G.G.,

A Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Nutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

B Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"T Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1314884; Tnfrsfla.

MGD; MGI:1314884; Tnfrsfla.

GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; IMP.

GO; GO:0006952; P:defenser response; IMP.

GO; GO:0006954; P:inflammatory response; IMP.

GO; GO:0007515; P:lymph gland development; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               which initiates the subsequent cascade of caspases (aspartate spignaling complex (DISC) performs caspase-8 protectolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis (By similarity). Substitution of TNF to the extracellular domain leads to homotrimerization. The aggregated death domains provide a novel molecular interface that interacts specifically with the death domain of TRADD. Various TRADD-interacting proteins such as TRAFS, RIP and possibly FADD, are recruited to the complex by their association with TRADD. This complex activates at least two distinct signaling cascades, apoptosis and NF-kappa-B signaling. Binds BAG4 (By similarity). Constitutively associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PURCE DNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
TNFSF1/Lymphotoxin-alpha. The adaptor molecule FADD recruits
caspase-8 to the activated receptor. The resulting death-inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type I membrane protein.
DOMALN: Both the cytoplasmic membrane-proximal region and the Cterminal region containing the death domain are involved in the interaction with TRPC4AP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, L26349; AAA59361.1; --
EMBL, M76656; AAA40465.1; --
EMBL, M88067; AAA40465.1; JOINED.
EMBL, M76655; AAA40465.1; JOINED.
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InterPro; IPR001368; TNFR C6.
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X59238;
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----SHCKKNEECMKLCLPPPLANVTNPQDSGTAVLLPLVILLGLCLLSFIFISLMCRY 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 PCTEPCGNSTCLVCPQDTFLAWENHHNSECARCOACDEQASQVALENCSAVADTRCGCKP 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 ICTVQLVGNSW------TPGY-PETQEALC----PQVTWSWDQLPSRALGPAAAP 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAHPORPDNADLAI----LYAVVDGVPPARWKEFMRFMGLSEHEIERLEMONGRCLRE 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSLVLLALLMGIHPSGVTGLVPSLGDREKRDSLCPQGKYVHSKNNSICCTKCHKGTYLVS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity.
By sim
Pfam; PF00020; TNFR c6; 4.
PROSITE; PSSO017; DEATH DOMAIN; 1.
PROSITE; PS00652; TNFR NGFR 1; 3.
PROSITE; PS50050; TNFR NGFR 2; 3.
Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane. SIGNAL 2 454 Tumor necrosis factor receptor CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.4%; Score 404.5; DB 1; Length 454; 27.2%; Pred. No. 4.7e-20; ive 56; Mismatches 191; Indels 93.
                                                                                                                                                                                                                                                                                                                                                                                          N-SMase activation domain (NSD).
Death.
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                                                                                                                                                                                  superfamily member 1A
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TNFR-Cys 3.
TNFR-Cys 4.
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TYPA, BAT. PRINK BAT. STANDARD; PRT; 461 AA. P. 22231; 201091, Q01193; CONTROL OF STANDARD; PRT; 461 AA. P. 22231; Ed. 13, Created)
DT. 10.100-1991; Ed. 13, Last sequence update)
DT. 10.100-1991; Ed. 13, PRT; Ed. 13, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 17.0%; Score 394.5; DB 1; Length 461;
Best Local Similarity 27.9%; Pred. No. 2.3e-19;
Matches 128; Conservative 55; Mismatches 202; Indels 73; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  SegHsd, strain LEW/NHsd, strain ACI/
SegHsd, strain DA/Bkl, strain F344/NHsd
and strain BN/SsNHsd).
EB23C05450FBD202 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          d (GlCNAC. . .) (Potential).
(in strain LEW/NHsd, strain ACI/
                                                                                                                                                        TWER-Cys 2.

TWER-Cys 4.

N-SMase activation domain (NSD).
Death.
By similarity.
Chorential).
N-linked (GlCNAc. ..) (Potential).
N-linked (GlCNAc. ..) (Potential).
N-linked (GlCNAc. ..) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                             SegHsd, strain DA/Bkl and strain F344/
NHsd).
                                                  Repeat; Signal; Transmembrane.
                                                                       Tumor necrosis factor receptor
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                                                                                    superfamily member 1A.
Extracellular (Potential).
                                                                                                                        Cytoplasmic (Potential).
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                                                                                                                                    TNFR-Cys 1.
TNFR-Cys 2.
                                                                                                             Potential
                                               Apoptosis, Glycoprotein, Receptor, Rep
SIGNAL 1 21 Potential
CHAIN 22 461 Tumor nec
SMART; SM00208; TNFR; 4.

ROGITE; PSS6017; DEATH DOMAIN; 1.

PROSITE; PS00652; TNFR NGFR 1; 3.

PROSITE; PS50050; TNFR_NGFR 2; 3.
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**MEDLINE=9827356; PubMed=9613449; DOI=10.1016/S0165-2427(97)00136-0; Lee B.-K., Kehrli M.E. Jr., Taylor M.J.; Lee B.-K., Kehrli M. Lee B.-K., Kehrli M. Lee B.-K., Kehrli M. Lee B.-K., Kehrli M. Lee B.-K., Taylor M. Lee B.-K., Kehrli M. Lee B.-K., Taylor M. Lee B.-K., Kehrli M. Lee B.-K., Ke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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R InterPro; IPR001489; Death.
InterPro; IPR0010289; DEATH like.
R InterPro; IPR001303; DEATH like.
R EnterPro; IPR001308; TNFR_c6.
R Pfam; PF00051; Death; 1.
R PRINTS; PR00351; 4FE45FRDOXIN.
R PARAT; SM00005; DEATH; 1.
R PROSITE; PS00017; DEATH DOMAIN; 1.
R PROSITE; PS00052; TNFR, 3.
R PROSITE; PS00050; TNFR, NGFR 1; 3.
R PROSITE; PS00050; TNFR, NGFR 2; 3.
R PROSITE; PS0050; TNFR, NGFR 2; 3.
R APOULOSIS; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOWAIN: Both the cytoplasmic membrane-proximal region and the C-terminal region containing the death domain are involved in the interaction with TRPC4AP (By similarity).
SIMILARITY: Contains 1 death domain.
SIMILARITY: Contains 4 TNFR-Cyg repeats.
                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
17-Umor necrosis factor receptor superfamily member 1A precursor (p60)
(TNF-R1) (TNF-R1) (p55).
Name=TNFRSF1A, Synonyms=TNFR1;
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                     471
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                                                                                                                                                                     STANDARD;
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SIGNAL
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TISSUE=Placenta;
MEDLINE=90235285; PubMed=2158863;
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                                                                                                                                                                                                                                                                                                                                                 Cell 61:361-370(1990).
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                                                                                                                                                                                    TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 KPGWFVECQVSQCVSSSPFYCQPCLDC--GALHRHTRLLC-SRRDTDCGTCLPGFYEHGD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 KCISC----HDCKNKECEKLCPTRPSTGKDSQDPGTTVLLPLVIVFGLCLASFASVVLA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: | | :: | 333 CRYQR-WKPKLYSIICGQSTLVKEGEPELLVPAPGFNPTTTICFSSTPSSSPVSIPPYIS 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 LGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAVYAALERMGLDGCVEDL 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 GCVSCPTSTLGSCPER-CAAVCGWR------QMFWVQVLLAGLVVPLLLGATLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 VAAALLLVLLGARAQGGTRSPRCDCAGDF------HKKIGLFCCRGCPAGHYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.7%; Score 387.5; DB 1; Length 471; 26.9%; Pred. No. 7.3e-19; ive 47; Mismatches 186; Indels 121; Gaps
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(GlcNAc. . ) (Potential)
(GlcNAc. . ) (Potential)
                                                                                                                                                               N-SMase activation domain (NSD).
Death.
necrosis factor receptor
                                Extracellular (Potential).
                                                                    Cytoplasmic (Potential).
TMFR-Cys 1.
TMFR-Cys 2.
TMFR-Cys 3.
TMFR-Cys 4.
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51367 MW;
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Matches 130;
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DISULFID
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STANDARD;

TRIA HUMAN P19438;

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MEDLINE=91090841; PubMed=1702293;
Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
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factor-binding protein.";
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MEDLINE=91006021; PubMed=1698610;
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"Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor receptor superfamily member 1A precursor (p60)
Tumor necrosis factor (D50) (CD120a) (COntains: Tumor necrosis factor binding protein 1 (TBP1)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-90235284; PubMed-2158862; Lohm H.-W., Gentz R., Brockhaus M., Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Leeslauer W., Tabuchi H., Leeslauer W., "Molecular cloning and expression of the human 55 kd tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND VARIANTS LEU-75 AND GLN-121.
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Rajkumar N.R., Toth B.J., Yi Q., Nickerson D.A.,
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FHCRC, Seattle, WA (URL: http://pga.gs.wachington.edul.";
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                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.; "Cloning of human tumor necrosis factor (TNR) receptor cDNA and expression of recombinant soluble TNR-binding protein."; Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92250049; PubMed=1315717;
Fuchs P., Strehl S., Dworzsk M., Himmler A., Ambros P.F.;
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localization to chromogome 12p13.";
                                                                                                       binding protein 1 (TBP1)].
Name=TNFRSF1A, Synonyms=TNFAR, TNFR1;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Placenta;
MEDLINE=91017509; PubMed=2170974;
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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A popkins R.F., Jordan H., Moore T., Mars J., Haibh F.,
Butchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldow M.F., Carninci P., Frange C.,
A Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
A Basa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boask S.A., McKernan R.J., Makek J.A., Gubbs R.A.,
AN Manna D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Madan A., Young A. Schentz J., Myers R.M.,
Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Marra M.A.,
Butterfield Y.S.N., Marywinski M.I., Marywinski M.I.,
Butterfield Y.S.N., Marywinski M.I., Marywinski M.J.,
Bu
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Engelmann H., Novick D., Wallach D.;
"Two tumor necrosis factor-binding proteins purified from human urine.
"Two tumor netrosis factor-binding proteins purified trom human urine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99213501, PubMed=10199409; DDI=10.1016/S0092-8674(00)80721-7; MEDLINE=99213501, PubMed=10199409; DDI=10.1016/S0092-8674(00)80721-7; McDermott M.F., Aksentievich I., Galon J., McDermott E.M., Ogunkolade B.W., Centola M., Mansfield E., Gadina M., Karenko L., Pettersson T., McGarthy J., Frucht D.M., Aringer M., Torosyan Y., Toropy A.-M., Wilson M., Karaarslan H.M., Wan Y., Todd I., Wood G., Schlingen R., Kumazajeewa T.R., Cooper S.M., Vella J.P., Amos C.I., Mulley J., Quane K.A., Molloy M.G., Rnaki A., Powell R.J., Hitman G.A., OʻShea J., Kastner D.L., Germine mutations in the extracellular domains of the 55 kDa TNF receptor, TNFR1, define a family of dominantly inherited
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99115917; PubMed=9915703; DOI=10.1126/science.283.5401.543; Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.; Prevention of constitutive TNF receptor 1 signaling by silencer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      necrosis factor receptors.";
J. Biol. Chem. 265:1531-1536(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97094982; PubMed=8939750;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Structure 4:1251-1262(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 283:543-546(1999).
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75 PGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYR 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74
                                                                                                                                                                                             VARIANTS FHF SER-99 AND PRO-121.

PubMed=13130484; DOI=10.1002/art.11215;

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associated periodic syndrome phenotypes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 EC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 LIELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPONNSICCTKCHKGTYLYNDCPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 PCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFV
                                         Aksentijevich I., Galon J., Soares M., Mansfield E., Hull K., Oh H.-H., Goldbach-Mansky R., Dean J., Athreya B., Reginato A.J., Henrickson M., Pons-Estel B., O'Shea J.J., Katner D.L.; "The tumor-necrosis-factor receptor-associated periodic syndrome: new mutations in TNFRSF1A, ancestral origins, genotype-phenotype studies, and evidence for further genetic heterogeneity of periodic fevers."; Am. J. Hum. Genet. 69:301-314(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 LLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCCRGCPAGHYLKAPCTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.1%; Score 374; DB 1; Length 455;
28.3%; Pred. No. 6.1e-18;
tive 49; Mismatches 183; Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
SUBCELLUIAR LOCATION: Type I membrane protein and secreted.
SUBCELLUIAR LOCATION: Type I membrane protein and secreted.
DOWAIN: The domain that induces A-SMASE is probably identical to the death domain. The N-SMASE activation domain (NSD) is both necessary and sufficient for activation of N-SMASE.
DOWAIN: Both the cytoplasmic membrane-proximal region and the C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=14610673; DOI=10.1007/800431-003-1338-0;
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"Tumour necrosis factor receptor-associated periodic syndrome with a
             VARIANTS FHF GLN-51; SER-59; GLY-62; LEU-75; GLY-115 AND GLN-121.
                                                                                                                                                                                                                                                                                                                                                                                                               Arthritis Rheum. 48:2632-2644 (2003).
                                 PubMed=11443543;
Aksentijevich I., Galon J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT FHF SER-99.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

Le Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: Receptor for INFSF6/FASL. The adaptor molecule FADD

recruits caspase-8 to the activated receptor. The resulting death-
inducing signaling complex (DISC) performs caspase-8 proteolytic

activation which initiates the subsequent cascade of caspases

(aspartate-specific cysteine proteases) mediating apoptosis. FAS-
mediated apoptosis may have a role in the induction of peripheral

colerance, in the antigen-stimulated suicide of mature T-cells, or

both (By similarity).

- SUBCELULAR LOCATION: Type I membrane protein.

- SUBCELULAR LOCATION: Type I membrane protein.

- DOMAIN: Contains a death domain involved in the binding of FADD,

and maybe to other cytosolic adaptor proteins.

- SIMILARITY: Contains 1 death domain.
                             183 TLGS-CPERCAAVC-----GWRQMFWVQVLLAGLVVPLLLGATLTYTYR----- 225
                                                                                                                                                                                                                                   278 GNSWTPGYPETQEALCPQVTWSWDQL------PSRALGP--AAAPTLSP----- 318
                                                                                                                                                                                                                                                                ::||
--TFTPS------DWANLRAASVSREMAPPYQGAGPILSAAPASSPISTPVQ 329
                                                                                                                                                                                                                                                                                                                                        -----ESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR 370
                                                                                                                                                                                                                                                                                                                                                                     186 KKNTECTKLCVPIVETVKDPQDPGTTVLLPLVIFFGICVLSFSIGLMCRYQRRKSKLFSI
                                                                                                                                 ---HCWPHK-----PLVTADEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D., "Expression of apoptosis-associated genes in hibernating and stunned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
(CD95 antigen).
                                                                                                                                                                                 246 VCGKSTPTKEGEPQPLATG----PGFSPIPSP---SPTFTPSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae; Sus,
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                       371 -FRDQQYEMLKRWRQQQP---AGLGAVYAALERMGLDGCVEDLRSRL 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         386 CLREAHYSMLAAWRRRTPRREATLELLGRVLRDMDLLGCLEDIEEAL 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000488; Death.
InterPro; IPR011029; DEATH like.
InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=TNFRSF6; Synonyms=APT1, FAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Created)
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                                                                                                                                                                                                                                                                                                                                        319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273 TVQLVGNSWTPGYPETQEALCPQVTWSWDQLPSRALGP-------AAAPTLSP- 318
                                                                                                                                                                                                                                              339 QKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGRCLRE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---AHTLLAPPDSSEKIC 272
                                                                                                                                                    S----SSTYTPGD-----CPNFA----APRREVAPPYQGADPILATALASDPIPNPL 338
                                                                                                                                                                                                      ---ESPAGSPAMMLOPGP-QLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRD 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 EPCGNSTCLVCPQDIFLAWENHHNSECARCOACDEQASQVALENCSAVADIRCGCKPGWF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 VECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCPTS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---QYRYYWSETHFQCLNCSLC--LNGTVQISCKETQNTVCTCHAGFFLRGNECVSCVNC 185
                                               239 -WKSKLYSIVCGKSTPEKEGELEGTTTKP---LAPNPSFSPTPGFTPTLGFSPVPSSTFT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Felis silvēstris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21455403; PubMed=11531421; DOI=10.1006/viro.2001.1042; Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.; Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.; infered cell death in feline immunodeficiency virus-infected cells is mediated by the caspase cascade."; Virology 287:446-455(2001).

EMBL; ABOS1103; BAB55455.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.7%; Score 365; DB 2; Length 446; 27.0%; Pred. No. 2.5e-17; tive 45; Mismatches 184; Indels 112;
                                                                                                                                                                                                                                                                                                        374 QQYEMLKRWRQQQP---AGLGAVYAALERWGLDGCVEDLRSRL 413
                                                                                                                                                                                                                                                                                                                                        217BD331DD8A74AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tumor necrosis factor type I.
227 CWPHK-----PLVTADEAGMEALTPPPATHLSPLDS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005515; F:protein binding; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007165; P:signal transduction; IEA.
INCEPPRO; IPR000345; CytC heme_BS.
INCEPPRO; IPR001029; Death.
INCEPPRO; IPR001029; DEATH like.
INCEPPRO; IPR006209; EGF like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
PROSITE; PS50017; DEATH DOMAÏN; 1.
PROSITE; PS01186; EGF 2; UNKNOWN 1.
PROSITE; PS00652; TNFR NGFR 1; 3.
PROSITE; PS50050; TNFR NGFR 2; 3.
SEQUENCE 446 AA; 49563 MW; 217BD331DD8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00531; Death; 1.
Pfam; PF00020; TNFR C6; 3.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=TNFR I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Simi
hes 126;
                                                                                                                                                                                                      319
                                                                                                                                                    295
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Matches
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Q95ND3
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GNFCCQLCPPGTKKKADCTSNEGKPDCEPCQEGEEYTDKSHFSSKCRRCSLCDGEHGLEV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 GLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||| :: |::|| |:: :|| :: :|| :: :|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |::|| |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 YRHCWPHKPLVTADEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 GYPETQEALCPQVTWSWDQLPSRALGPAAAP----TLSPESPAGSPAMMLQPGPQLYD 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYDK------STALIPEGVPMNFSDVDISKYIPT------ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 LENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 TCLPGFYEHGDGCVSCPTSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Kidney,
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshlywir S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.7%; Score 226; DB 2; Length 319;
Best Local Similarity 21.0%; Pred. No. 8.2e-08;
Matches 73; Conservative 42; Mismatches 103; Indels 130; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 VMDAVPARRWKEFVRTLGLREAEIEAVEVE-IGRFRDQQYEMLKRWRQ 384
GO; GO:0006915; P:immune response; IEA.

GO; GO:0007165; P:immune response; IEA.

GO; GO:0007165; P:immune response; IEA.

InterPro; IRR00488; Death.

InterPro; IRR008063; Fas receptor.

InterPro; IRR008063; Fas receptor.

InterPro; IRR008063; Fas receptor.

InterPro; IRR008063; Fas receptor.

Pfam; PF00520; TWFR C6; 2.

R PRINTS; PR006009; TWFR, 1.

R SWART; SW000009; TWFR; 1.

R SWART; SW000009; TWFR; 1.

R PROSITE; PSS0017; DEATH DOMAIN; 1.

R PROSITE; PSS0017; DEATH DOMAIN; 1.

R PROSITE; PSS0017; DEATH DOMAIN; 1.

R PROSITE; PSS0052; TWFR, MGFR_1; UNKNOWN_1.

R PROSITE; PSS0052; TWFR_MGFR_1; 0.06FA0033B1846591 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 LRRYKKHR---------
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Last sequence update)
Last annotation update)
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Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 ACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 LCSRRDTDCGTCLPGFYEHG--DGCVSCPTSTLGSCPERCAAVCGWRQMFWVQVLLAGLV 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------EHGVIENCT--PISNT-KCREVFQSAGSRSNLHWLWALLILIP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 DCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQ 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.7%; Score 247.5; DB 1; Length 332;
Best Local Similarity 30.3%; Pred. No. 2.7e-09;
Matches 56; Conservative 23; Mismatches 67; Indels 39; Gaps
Pfam; PF00020; TNFR_C6; 3.
PRINTS; PR01680; FASRECEPTOR.
SWART; SM00005; DEATH; 1.
SMART; SM01005; TNFR, 1.
PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS50052; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                        Cytoplasmic (Potential).
TURR-Cys 1.
TURR-Cys 2.
TURR-Cys 3.
Death.
By similarity.
No similarity.
By similarity.
Whinked (GlorNac. . . ) (Potential).
No linked (GlorNac. . . ) (Potential).
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Oydcolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                             Tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Isono T., Tanbe Y., Nagano Y., Seto A.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AB0212998; BAA78430.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO:0016620; C:membrane; IEA.
GO:0005515; F:protein binding; IEA.
GO:0004888; F:transmembrane receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                           superfamily member 6.
Extracellular (Potential)
Potential.
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 AA;
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                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRRLGVSEQNIDRAEHDHRNCKDAQYQMLKVWSDGGSGGGNNVVPYDQIQMLMSTLKDMC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --QVSQCVSSSPFYCQPCLDCGALH----RHTRLLCSRRDTDCGTCLPGFYEHGDGC--- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --VSCP----TSTLGSCPERCAAVCGWRQMFWVQVLLAGLIVVPLLLGATLTYTYRHCWPH 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 KPLVTADEAGMEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQE 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRTLGLREAEIEAVEVEIGRFRDOQYEMLKRWRQQQPAG-----LGAVYAALERMG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CKTSIPPVFFTSTKSNSPEDTVPK-----IVVPVCASIMVLSLAIFMAYEGIRHWRK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGNKTMKGNCLENEYWNKEG-FCCDKCHQGYKLKQECSAENMRSKCEKCDEGTYLEQAN-82
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Blakesley R.W., Touchman A.C., Shewchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; Green E.D., Grimwond J., Schmitz J., Myers R.M., Butterfield Y.S., Wrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTRSPRCDC-AGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 ALCPQVTWSWDQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HNSECARCQACDEQASQVALENCSAVADTRCGCKP------GWFVEC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.6%; Score 223.5; DB 2; Length 389;
larity 21.8%; Pred. No. 1.5e-07;
Conservative 60; Mismatches 158; Indels 119,
                                                                                                                                                                                                                                              Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO64241, AAH684241, 252;
ZFIN; ZDB-GENE-040426-2252; zgc:85914.
GO; GO:0005515; F:protein binding; IEA.
GO; GO:0007165; P:signal transduction; IEA.
R InterPro; IPR001450; 4Fe4S ferredoxin.
R InterPro; IPR001488; Death.
R InterPro; IPR01029; DEATH like.
R InterPro; IPR011029; DEATH like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00511; Death; 1.
Pfam; PF00037; Fer4; 1.
Pfam; PF00020; TNPR. c6; 3.
SMART; SM00006; DBATH; 1.
SMART; SM00006; DBATH; 1.
SMART; SM00006; DRATH; 1.
PROSITE; PS00190; CYTOCHROME C; UNRNOWN 1.
PROSITE; PS00652; TNFR. NGFR 1; UNRNOWN 2.
PROSITE; PS00652; TNFR. NGFR 1; UNRNOWN 2.
SEQUENCE 389 AA; 44099 MW; 9EB46F454519FB3C CRC64;
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Search completed: June 27, 2005, 13:40:20 Job time : 179 secs

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1 MEQRPRGCAAVAAALLLVLL......ERMGLDGCVEDLRSKLQRGP 417
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Aab84941 Amino aci	Adh50948 Human dea	Aaw64486 Human DR3	Abg73995 Human Apo	Abg73862 Human foe	Adlisoil Human WSL	Abm84914 Human dia	Abm84915 Human dia	Aaw31516 Death dom	Aaw95537 Death dom	Aab36264 Human dea	Adg88379 Human DR3	Adl27891 Human Dea	Aab01337 TNF recep	Aab50918 Human PRO	Aaw57046 Mouse apo	Human	Adl15010 Human WSL		~
AAB84941	ADH50948	AAW64486	ABG73995	ABG73862	ADL15011	ABM84914	ABM84915	AAW31516	AAW95537	AAB36264	ADG88379	ADL27891	AAB01337	AAB50918	AAW57046	ADL15009	ADL15010	AAW26708	ABG73992
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418	418	833	416	416	417	451	450	428	428	428	428	428	426	343	411	253	218	181	181
100.0	100.0	100.0	99.4	99.4	99.3	98.7	98.0	97.6	97.6	97.6	97.6	97.6	93.8	80.2	60.4	50.1	45.3	45.2	45.2
2323	2323	2323	2308.5	2308.5	2306	2292	2277.5	2267	2267	2267	2267	2267	2179.5	1862	1404	1164	1052.5	1051	1021
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Death domain containing receptor; DR3-V1; human; apoptosis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                          Death domain containing receptor polypeptide(s) DR3 and DR3-V2 - for activation of apoptosis and NP-kappaB, antagonists can be used to treat inflammatory diseases.
                                                                                                                                                                                                                                                                                                                                                             Yu G, Ni J, Dixit VM, Gentz RL, Dillon PJ;
                                                                                                                                                                       /note= "extracellular domain"
202. .224
                                                                                                                                                                                                   225. .417
/note= "intracellular domain"
                                                                                                                                                                                           'note= "transmembrane domain"
                                                                                                                                                                                                                       342. .408
/note= "death domain"
                                                               Death domain containing receptor DR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 75-77; 108pp; English.
                                                                                                                                            1. .24
/label= Sig_peptide
                                                                                                                                   Location/Qualifiers
        AAW31517 standard; protein; 417 AA
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                                              (first entry)
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                                                                                                                                                                                                                                                     WO9733904-A1
                                              02-MAR-1998
                                                                                                                Homo sapiens
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                                                                                              NF-kappaB
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CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel member of the tumour accrosis factor receptor family. Its amino acid sequence was deduced from a CDNA clone (see AAT89427) isolated from a did sequence was deduced from a CDNA clone (see AAT89427) isolated from a HVVEC CDNA library. Related death domain containing receptor DR3-VI (see AAW31516) has also been identified. Recombinant full-length or domain of DR3 can be extracellular, transmembrane, intracellular or death domain of DR3 can be expressed in transformed host cells. These polypeptides can be used to treat diseases and disorders associated with the inhibition of apoptosis, or to screen for modulator compounds. Antagonists, such as antibodies rasised against DR3-V1, can be used to treat diseases and disorders associated with increased apoptosis and for treatting inflammatory diseases and disorders
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                 protein comprises human death domain containing
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/note= "extracellular domain"
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/label=_Sig_peptide
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                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 417; Conservative
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into incorp poptoric activity in mammalian cells purposes. Its amino acid sequence was deduced from a human foetal heart cDNA clone (see AAF91180).

Competence was deduced from a human foetal heart cDNA clone (see AAF91180).

The N-terminal 181 amino acids of Apo-3 are identical to the sequence of another novel apoptosis polypeptide, Apo-211 (see AAF87679). Also claimed are: polypeptides comprising the extracellular or death domain of Apo-3; chimeric molecules comprising Apo-1 fused to a heterologous amino acid sequence; antibodies that bind to Apo-3 or its extracellular domain; cells; a non-human transgenic animal containing cells that express contoining an altered Apo-3; and a non-human knockout animal containing cells having an altered Apo-3 gene. Apo-3 can be used to induce apoptosis or NF-kB induction or JNK activation for therapeutic purposes. Apo-3-1gG fusion proteins can be used to inhibit apoptosis or used as immunogens for anti-Apo-3- antibody production. Apo-3 or Apo-2011 can also be used as assay standards. The animals can be used in drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This novel polypeptide, designated Apo-3, is a protein that stimulates or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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 /note= "transmembrane domain"
                   225. .417
/note= "intracellular
                                                    338. .417
/note= "death domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 19; Page 46-48; 70pp; English.
                                                                                                                                                                                     97WO-US005230.
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96US-00710802.
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The invention provides nucleotide sequences encoding death domain containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is contained in ATCC deposition No. 97757. Recombinant vectors comprising the nucleic acid sequences and optionally the leader sequences are used for the recombinant production of the proteins. The present sequence represents the amino acid sequence of a death domain containing receptor
MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
                                                                                                                                                               DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
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                                                                                                                                                                                                                                                                                   361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Death domain containing receptor polypeptide (DR3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Death domain; receptor; DR3-V1; DR3; recombinant.
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/note= "signal peptide"
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/note= "mature protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAW95538 standard; protein; 417
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96US-0028711P.
97US-0037341P.
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Best Local Similarity 100.0
Matches 417; Conservative
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06-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is the human apoptosis inducing receptor (AIR) of the invention. AIR is a Type I transmembrane protein, soluble forms of which can be used to regulate cell death in a therapeutic setting. Soluble AIR can be used to requist of block apoptosis or AIR-expressing cells, or to screen agonists or antagonists of AIR activity. The cytoplasmic domain of AIR can be used to develop assays for inhibitors of AIR-induced cell death, which is useful to regulate cell death in a therapeutic setting as well as in vitro. Agonists of AIR activity can be used to kill tumour cells that express AIR, or I cells expressing AIR in autoimmune diseases
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TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240
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    which is Type I transmembrane

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                                                                                                                                                                                                                                                                                                                                                                                                                      Apoptosis inducing receptor; AIR protein; human; cell death regulator; Type I transmembrane protein; tumour cell death; autoimmune disease;
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100.0%; Pred. No. 1.3e-161;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                           Human apoptosis inducing receptor.
                                                                                                                                                                                                                                   AAW57045 standard; protein; 417
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N-PSDB; AAV28700.
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                                                                                         CTEPCGNSTCLVCPQDTFLAWENHINSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                                                                                                                                                                                                                                  TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240
                                                                                                                                                                                                                                                                                                                                                    241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
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                                                                                                                                                                                                                                                                                                                                                                                                              DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
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                                                                  CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                                                                                                                     WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour necrosis factor receptor; TR3; DR3; Apo3; WSL-1; LARD; agonist; antagonist; screening; human; Alzheimer's disease; AIDS; cancer; inflammation; arthritis; septicaemia; autoimmune disease; psoriasis; inflammatory bowel disease; transplant rejection; graft versus host disease; infection; stroke; ischaemia; acute respiratory disease syndrome; restenosis; brain injury; bone disease; atherosclerosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying agonists and antagonists of tumor necrosis factor related receptors TR1, TR3 and TR5, and of ligand TL3, useful for treatment of cancer, AIDS, Alzheimer's disease, bone disease etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 IEAVEVEIGRFRDOOYEMLKRWROOOPAGLGAVYAALERMGLDGCVEDLRSRLORGP 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERWGLDGCVEDLRSRLQRGP 417
Disclosure; Page 12-13; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour necrosis factor receptor TR3
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to the receptors or ligand, and which activate (agonist) or inhibit activation of (antagonists) TR1, TR3, TR5 or TL3. A screening kit for identifying agonists, antagonists, ligands, receptors, substrates, enzymes etc. for TR1, TR3, TR5 or TL3 polypeptides is provided. The agonists and antagonists are useful for treatment of chronic and acute inflammation, arthritis, septicaemia, autoimmune disease e.g. inflammatory bowel disease, psoriaats, transplant rejection, graft versus host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, restencesis, brain injury, AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders), atheroscierosis, Alzheimer's disease, etc., caused by imbalance of TR1, TR3, TR5 or TL3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 2323; DB 2; Length 417; 100.0%; Pred. No. 1.3e-161; ive 0; Mismatches 0; Indels 0.
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This invention relates to a method of diagnosing chronic rheumatoid arthritis by digesting human genomic DNA with BCORI and hybridising it with a probe for the DNA encoding the present protein which is a rheumatoid arthritis associated transmembrane protein. The method is used for the diagnosis of chronic rheumatoid arthritis, and for developing new
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                                                                                                                                                                                                                                                                                                       Diagnosing rheumatoid arthritis by probing digested human genomic DNA or comparing expression of mRNA or polypeptide of a region of transmembrane
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 Rheumatoid arthritis; transmembrane protein; human
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                                                                                                                              01-NOV-2000; 2000WO-JP007690.
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                                                                                                                                                                                            SHIO/) SHIOZAWA
                                                                                                                                                                                                                                                                         N-PSDB; AAH27782
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                                                               WO200132921-A2
                                   Homo sapiens
                                                                                                                                                              01-NOV-1999;
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                                                                                               10-MAY-2001
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                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences for two death domain containing receptors, designated DR3 and DR3-V1. These receptors are involved in apoptosis, and the sequences given can be used in the treatment of cancers, inflections, cardiovascular disorders such as arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms and congenital heart defects, neurodegenerative diseases including Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple sclerosis, arthritis, diabetes, Graves disease, asthma and psoriasis, and to promote angiogenesis and wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQBALCPQVTWSM 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                        Treating graft-versus-host disease, cancer, immunodeficiency or an autoimmune disease comprising administering an antibody to Death Domain Containing Receptor proteins and a second therapeutic agent.
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                                                                                                             Dixit VM;
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                                                                                                             Gentz RL,
UNIV MICHIGAN
                                           GENTZ R L.
DILLON P J.
DIXIT V M.
                                                                                                                                         WPI; 2000-687263/67.
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                                                                                                                                                              N-PSDB; AAC68777
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 417 AA;
                                                                                                             Ni J,
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AAU86139 standard; protein; 417 AA
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99US-0145698P.
99US-0146222P.
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99WO-US028301.
99WO-US028634.
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99WO-US021090
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                                                                                 (first entry)
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Best Local Similarity 100.
Matches 417; Conservative
                                                                                                      Human PRO779 polypeptide
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Wood WI;
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                                                                                                                                                              neuroprotective
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                                                                                                                                                                                                                                                                                                                                                                           17-AUG-1999;
31-AUG-1999;
01-SEP-1999;
15-SEP-1999;
30-NOV-1999;
01-DEC-1999;
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26-JUL-1999;
28-JUL-1999;
                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                            02-JUN-1999;
22-JUN-1999;
22-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watanabe CK,
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                                                                                 15-JUL-2002
                                                                                                                                                                                                                                                                                       11-MAR-1999
11-MAY-1999
                                                                                                                                                                                                                                26-JUL-2001
                       AAU86139
              RESULT
                                               with rheumatoid arthritis. Certain mutations in the gene can be linked to the disease. The sequences can be used to evaluate disease onset and its possibility and to provide therapy and remedies. The present sequence is a protein described in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240
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                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to the human DR3 gene, which is associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                         Genomes, particularly DR3 genomic DNA, participating in rheumatoid arthritis via mutation, useful in evaluating disease onset and its possibility and providing therapy and remedies.
                      Human rheumatoid arthritis associated DR3 gene related protein #1.
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                                            Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 2323; DB 5; Length 417; 100.0%; Pred. No. 1.3e-161; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 69-70; 84pp; Japanese.
                                                                                                                                                                     24-OCT-2000; 2000JP-00324296.
27-MAR-2001; 2001JP-00090546.
30-MAR-2001; 2001JP-00099990.
                                                                                                                                                 24-OCT-2001; 2001WO-JP009313
22-AUG-2002 (first entry)
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Best Local Similarity 100.
Matches 417, Conservative
                                                                                                                                                                                                                  (NEWI-) NEW IND RES ORG. (SHIO/) SHIOZAWA S.
                                                                                                                                                                                                                                                    Shiozawa S, Konishi Y;
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N-PSDB; AAL47186.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 417 AA;
                                                                                                    WO200234912-A1
                                                       therapy
                                                                                Homo sapiens.
                                                                                                                          02-MAY-2002
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!uman; PRO; benign tumour; malignant tumour; lymphoid malignancy;
leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder;
inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumors, leukemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders.
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Stone DM;
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Smith V,
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100.0%; Pred. No. 1.3e-161;
iive 0; Mismatches 0;
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Pan J, Pitti RM, Roy MA,
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ABU08252 standard; protein; 417
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        WPI; 2003-147110/14.
N-PSDB; ABX15842.
                                                                                                                                                                                                                                                            Sequence 417 AA;
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                                                                                                                                                                                                                                           invention
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                                                                                                   TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240
                                                                                                                                     MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
                                                                                                                                                                       DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
                                               61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                                                  121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
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                               CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG
         1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
                                                                                                                                                                                                                                                                                                                                      APO-3; human; apoptosis; monoclonal antibody; cytostatic; cancer; autoimmune; inflammatory; neurodegenerative disease.
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/note= "Extracellular domain"
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/note= "Transmembrane domain"
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/note= "Intracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "N glycosylated"
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/label= Signal_peptide
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96US-00710802.
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                                                                                                                                                                                                                                                                                                                        Human Apo3 protein.
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23-SEP-1996;
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This invention relates to an isolated monoclonal antibody comprising an antigen binding site which binds to an Apo-2 ligand inhibitor (Apo-2LI) polypeptide and an antibody that binds the Apo3 protein. The antibodies of the invention may have cytostatic activity and may act as activators of the invention may have cytostatic activity and may act as activators or stimulator of apoptosis in cancer cells, as blockers of excessive apoptosis or of the autoimmune/inflammatory effects of Apo-3 resulting from nuclear factor (NF) kappaB activation or C-Jun-amino-terminal kinase (JNK) activation. The anti-Apo-2 ligand inhibitor is useful in thermodegenerative disease), or to block potential autoimmune/ cells and may be used to block excessive apoptosis (for example in neurodegenerative disease), or to block potential autoimmune/ cells and may be used in diagnostic assays for Apo-2LI or Apo-3, e.g. cetecting Apo-2LI or Apo-3 resulting from nuclear factor (NF)-kappaB activation or C-Jun-amino-terminal kinase (JNK) activation. The antibody may also be used in diagnostic assays for Apo-2LI or Apo-3, e.g. cerum, or for affinity purification of Apo-2LI or Apo-3 from recombinant cell culture or natural sources. The present sequence represents the human Apo3 protein which was used to generate the antibody of the
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Novel isolated monoclonal antibody useful for activating or stimulating apoptosis in cancer cells, comprises an antigen binding site which binds to an Apo-2 ligand inhibitor polypeptide or to an Apo-3 polypeptide.
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                                                                                                                                                           Claim 1; Fig 4; 48pp; English
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CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                  WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                      MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nuclear factor kappa B; NF-kappa B; Alzheimer's disease; AIDS; tumour necrosis factor receptor; acquired immunodeficiency syndrome; Parkinson's disease; amyotrophic lateral sclerosis; multiple sclerosis; retinitis pigmentosa; cerebellar degeneration; aplastic anaemia; myocardial infarction; stroke; reperfusion injury; toxin-induced liver disease; cancer; lupus; herpes virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                               361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERWGLDGCVEDLRSRLQRGF 417
                                                                             TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG
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2 of the specification"
                                                                                                                                            TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG
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/note= "Death domain. This domain is specifically
claimed in claim 3 of the specification"
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specifically claimed in claim
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/note= "Mature Apo-3 protein"
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an new isolated biologically active Apo-2LI or Apo-3 having at least 80 % sequence identity with native sequence Apo-2LI or Apo-3 appearing as ABU08251 and ABU08225. Also included are a chimaeric molecule comprising the Apo-2LI fused to a hererologous amino acid sequence; a dimer molecule comprising a first Apo-2LI and a second Apo-2LI, an antibody that binds to Apo-2LI or Apo-2LI and a second Apo-1LI, an antibody that binds to Apo-2LI or Apo-2LI and a second correctly a vector comprising the nucleic acid, a host cell comprising the vector, a method of producing Apo-2LI and a non-human (transgenic or Knockout) animal that contains cells that express nucleic acid encoding Apo-3 or cells having an altered gene encoding Apo-3. Apo-2LI or Apo-3 are involved in apoptosis (programmed cell death) which is implicated in Apo-3 or cells having an altered gene encoding Apo-3. Apo-2LI or Apo-3 are involved in apoptosis (programmed cell death) which is implicated in Apo-3 are also variation and takens cerebellar degeneration, reperfusion, reperfusion and takens sclerosis, multiple sclerosis, retinitis pigmentosa, aplastic anaemia, cerebellar degeneration, myocardial infarction, reperfusion injury and toxin-induced liver myocardial infarction, reperfusion injury and toxin-induced liver cancer. The gene for both proteins is located on chromosome 1936.3 Apo-2LI and Apo-3 are also useful for preparing a composition for treating cancer. The present sequence represents Apo-3
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                                      Human; Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; AIDS; acquired immunodeficiency syndrome; stroke; Alzheimer's disease; cancer; Parkinson's disease; amyotrophic lateral sclerosis; multiple sclerosis; retinitis pigmentosa; aplastic anaemia; cerebellar degeneration; myocardial infarction; reperfusion injury; toxin-induced liver disease; chromosome 1q36.3; programmed cell death.
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                                                                                                                                                                                                                                                                               1. .198
/label= Extracellular_domain
/note= "This domain is claimed in claim 26"
                                                                                                                                                                                                                                                                                                                                                                                                 /note= "This domain is claimed in claim 27"
                                                                                                                                                                                                                                                                                                                                                338. .417
/label= Death domain
                                                                                                                                                                                                                                                       Location/Qualifiers
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96US-0026943P.
97US-00829270.
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Matches 417; Conservative (
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Human Apo-3 protein.
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ABU10204 standard; protein; 417 AA.

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Towells of apoptosis are associated with diseases such as acquired immunodeficiency syndrome (AIDS), Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial infarction, stroke, reperfusion injury, and toxin-induced liver disease. The Apo-3 polypeptide is also useful in non-therapeutic applications such as in quantitative diagnostic assays as a control against which samples containing unknown quantities of Apo-3 may be prepared, in generating antiques, and in competitive-type receptor binding assays. The chimeric cechniques, and in competitive-type receptor binding assays. The chimeric molecule is useful therapeutically to inhibit apoptosis or nuclear factor kappa B (MP-kappa B) induction, or as an immunogen for producing anti-Apo-3 antibodies. The present sequence represents the polypeptide sequence of the human Apo-3 protein present in the foetal heart
                                                                                                                                                                                                                                                                                                                         The invention relates to an Apo-3 polypeptide having an extracellular domain (BCD) sequence and a death domain sequence. The Apo-3 polypeptide has been found to stimulate or induce apoptotic activity in mammalian cells. Human Apo-3 exhibits similarities to the tumour necrosis factor receptor (TNFR) family of polypeptides. The invention also relates to a reimeric molecule comprising an extracellular domain sequence comprising residues 1-198 of Apo-3 fused to a heterologous amino acid sequence. The Apo-3 polypeptide is useful therapeutically to induce apoptosis in mammalian cells. Decreased levels of apoptosis has been associated with conditions such as cancer, lupus, and herpes virus infection. Increased
                                                                                                                                              Novel isolated Apo-3 polypeptide useful for inducing apoptosis in mammalian cells, for generating antibodies, in affinity purification techniques, and in competitive-type receptor binding assays.
                                                                                                                                                                                                                                                                    Claim 1; Fig 8; 52pp; English.
                                                          WPI; 2003-173840/17.
N-PSDB; ABX15464.
Ashkenazi AJ;
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Sequence 417 AA;

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                                      Gaps
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100.0%; Score 2323; DB 6; Length 417; 100.0%; Pred. No. 1.3e-161; ive 0; Mismatches 0; Indels 0.
                   Best Local Similarity 100.
Matches 417; Conservative
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RESULT 13 ABU10204

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The invention relates to an isolated Apo-3 polypeptide. The Apo-3 polypeptides are useful for stimulating or inducing apoptotic activity in mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy techniques. The Apo-3 chimeric molecules are useful for inhibiting apoptosis, or as immunogens used in generating antibodies. The antagonistic antibodies may be used to block excessive apoptosis, for instance in neurodegenerative disease, or to block potential autoimmune/inflammatory effects of Apo-3 resulting from NF-kappas activation. The nucleic acid sequences are useful as diagnostics for tissue-specific kryping, for preparing Apo-3 polypeptides, or for generating transgenic or knockout animals. The transgenic or knockout animals are useful in developing and screening of therapeutically useful reagents. The present sequence represents the amino acid sequence of human Apo-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Apo-3 polypeptides, useful for stimulating or inducing apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo
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                                                                                                                      Human; Apo-3; apoptosis; gene therapy; inflammation; cancer;
neurodegenerative disease; immunosuppresive; tissue typing.
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/label= Extracellular_domain
199. .224
/label= Transmembrane_domain
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/label= Intracellular_domain
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/label= Signal_sequence
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|abel= Mature_Apo-3
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97US-00928069.
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Best Local Similarity 100.
Matches 417; Conservative
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11-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENCEPTIN; obesity; lipid partitioning; lipid metabolism; insulin-like activity; free fatty acid oxidation; weight reduction; anorectic; antilipaemic; artistreriosolerotic; cardiant; antidiabetic; hypotensive; ophthalmological; neuroprotective; nephrotropic; obesity-related disease; insulin resistance; atherosoclerosis; atheromatous disease; heart disease; cardiac insufficiency; ocronary insufficiency; high blood pressure; hypertension; stroke; syndrome X; diabetes mellitus; hyperlipidaemia; hyperuricaemia; diabetic complication; microangiopathic lesion; ocular lesion; retinopathy; neuropathy; renal lesion.
                                                                                                                                                                                                                                                                                                                                                                                 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP
                                                                                                                                           TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG
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200. .222
/label = transmembrane_domain
223. .417
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116. .163
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164. .192
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/note= "Cys rich region"
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/label= GENCEPTIN
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/label= signal
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The present invention describes the use of an agonist or antagonist of GENCEPTIN activity for preventing or treating obesity. Also described is a method of screening for GENCEPTIN activity, for preventing or treating obesity. Also described is a method of screening for GENCEPTIN setty acid oxidation, and useful insulin-like activity, free fatty acid oxidation, and antarteriosclerotic, cardiant, antidiabetic, hypotensive, ophthalmological, neuroprotective and nephrotropic activities. GENCEPTIN can be used for treating or preventing obesity-related disease or disorders, e.g. obesity, insulin resistance, atherosalerosis, atheromatous disease, heart disease (e.g. cardiac insufficiency, toronary insulin the presents), hypertension, stroke, syndrome X, diabetes mellitus (type I and II), hyperlipidaemia and hyperuricaemia, also diabetic complications, e.g. micromagiopathic lesions, ocular lesions, retinopathy, neuropathy and renal lesions. The present sequence represents human GENCEPTIN, which is given in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New use of Genceptin agonists or antagonists for treating or obesity-related diseases or disorders.
                                                                     Leu"
   or Arg'
                                                                     or
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/note= "polymorphic amino acid Ala
                                                                  /note= "polymorphic amino acid Arg
                                                                                                                                    /note= "polymorphic amino acid Arg
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Matches 417; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 164. .181
/label= Cysteine-rich domain 4
/note= "This cysteine-rich domain is apparently truncated
in Apo-2LI and contains only 3 cysteines instead of 6."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated biologically active Apo-2LI or Apo-3 which has at least 80% sequence identity with native sequence Apo-2LI having 1-181 amino acids or Apo-3 having 1-417 amino acids, respectively. Apo-3 can be employed therapeutically to induce apoptosis or NF-kappaB or JNK mediated gene expression in mammalian cells. The Apo-3 chimeric molecules can be employed therapeutically to inhibit apoptosis; necrosis factor (NF)-kappaB induction, c-Jun N-terminal kinase (JNK) activation. Apo-2LI can be employed therapeutically to inhibit mammalian cell
                                                                                                                                                                                                                                                                                                            /note= "Specifically claimed in claim 4. Residues 1-181 of Apo-3 represent Apo2LI"
                              417
                                                                                                                                                                        human; Apo-2 ligand inhibitor; Apo-2L1; apoptosis; NF-kappaB; JNK; c-Jun N-terminal kinase; necrosis factor kappa B; chimeric molecule; tissue-specific typing; Apo-3; transgenic; affinity purification; competitive-type receptor binding assay.
        New isolated biologically active Apo-2LI or Apo-3 used to induce apoptosis in mammalian cells.
                                                                                                                                                                                                                                                                                                                                                                           16. 163
| Tabel = Cysteine-rich_domain_3
                                                                                                                                                                                                                                                                                                                                               'label= Cysteine-rich_domain_1
                                                                                                                                                                                                                                                                                                                                                                   Cysteine-rich_domain_2

    198
    Iabel= Extracellular_domain

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/label= Death_domain
                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                   ABG73824 standard; protein; 417 AA.
                                                                                                                                                     Human apoptotic protein, Apo-3.
                                                                                                                                                                                                                                                                                        |. .181
|abel= Apo-2LI
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96US-00710802.
97US-00828683.
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23-SEP-1996;
31-MAR-1997;
                                                                                                                                                                                                                                  Homo sapiens.
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apoptosis in vivo or ex vivo. Nucleic acid sequences encoding the Apo-3 or Apo-2LI may be used as a diagnostic for tissue-specific typing. The isolated Apo-2 an Apo-2LI may be used in quantitative diagnostic assays as a control against which samples containing unknown quantities of Apo-3 or Apo-2LI may be prepared. Apo-3 preparations are also useful in generating antibodies, as standards in assays for Apo-3 or Apo-2LI, in affinity purification techniques, and in competitive-type receptor fluorophores. Modified forms of the Apo-3, e.g. Apo-3 or Apo-3. In the conclusion assays when labelled with, e.g. radioiodine, enzymes, or fluorophores. Modified forms of the Apo-3, e.g. Apo-3-1gG chimeric and be used as immunogens in producing anti-Apo-3 antibodies. Nucleic acids which encode Apo-3 or its modified forms can also be used to generate either transgenic animals or knock out animals, e.g. mouse or rat, which, in turn, are useful in the development and screening of therapeutically useful reagents. The Apo-3 polypeptide stimulates or induces apoptotic activity in mammalian cells. The present sequence represents the human apoptotic protein, Apo-3 Residues 1.181 of Apo3 cepting applied or apoly a secreted or soluble form of Apo3
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le : 167 secs
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Matches 417; Conservative
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FAIS FAGE BLANK (USPTO)

Sequence

US-10-211-884-24 US-10-310-793-4 US-10-415-247-3 US-10-648-825-5 US-10-648-825-5 US-10-744-379-2 US-10-226-296-5 US-10-226-318-5 US-10-26-318-5 US-10-648-786-5 US-10-648-786-5

Sequence 5, Appli Sequence 7, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 15, Appli

0 US-09-114-889-2 5 US-10-189-189-2 5 US-10-189-189-2 1US-09-993-234-1 US-09-993-234-1 US-10-112-193-1 US-10-112-193-1 US-10-112-193-1 US-10-112-193-1 US-10-112-193-1 US-10-112-193-1 US-10-112-193-1 US-10-199-345-24

US-10-207-295-9 US-10-242-383-15 US-09-899-422-15 US-09-899-424-15 US-09-4898-234-15 US-09-792-356-15

US-10-252-408-4

ALIGNMENTS

US-09-970-532-2 US-09-887-879-15 US-09-992-964-15

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ADDRESSEE: Sterne, Ressler, Goldstein & Fox, P.L.C.
ADDRESSEE: Sterne, Ressler, Goldstein & Fox, P.L.C.
STREET: 1100 New York Ave., NW, Suite 600
STATE: 100 New York Ave., NW, Suite 600
STATE: DC
COUNTRY: USA
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,966
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: No. US20020009773A1 Yet Assigned FILING DATE: 06-FEB-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/0933966
Patent No. US20020009773A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Nix, Vishva
APPLICANT: Dixt, Vishva
APPLICANT: Dixt, Vishva
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE:
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Sequence 6, Appli
Sequence 10, Appl
Sequence 10, Appli
Sequence 4, Appli
Sequence 24, Appli
Sequence 24, Appli
                                                                                             June 27, 2005, 13:40:47; Search time 161 Seconds (without alignments) 996.003 Million cell updates/sec
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Sequence 5, 2
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                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA:*

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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-874-138-5
US-09-314-889-4
US-10-005-842-5
US-10-012-793-6
US-10-112-193-10
US-10-112-193-10
US-10-112-193-10
US-10-118-189-4
US-10-118-189-4
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Maximum Match 100%
Listing first 45 summaries
                                                                      protein search, using sw model
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seq length: 200000000
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Maximum DB E
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Query Match
Best Local Similarity 100.0
Matches 417; Conservative
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                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                     LENGTH: 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTEPCGNSTCLVCPQDTFLAWENHINSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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Patent No. US20020072091A1
GENERAL INFORMATION:
APPLICANT: Ni, Jan
APPLICANT: Yu, Guo-liang
APPLICANT: Yu, Guo-liang
APPLICANT: Yu, Guo-liang
APPLICANT: Nu, Guo-liang
APPLICANT: Nu, Guo-liang
CURRENT ROSE, 188.1310006
CURRENT APPLICATION NUMBER: US/99/874,138
CURRENT APPLICATION NUMBER: 09/565,009
PRIOR PILING DATE: 2001-06-06
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 1999-08-13
PRIOR PLING DATE: 1999-08-13
PRIOR FILING DATE: 1999-06-07
PRIOR PLING DATE: 1999-06-07
PRIOR PLING DATE: 1999-06-07
PRIOR PLING DATE: 1999-06-07
FILING DATE: 17-07-1996
FILING DATE: 17-07-1996
FILING DATE: 17-07-1996
FILING DATE: 17-07-1996
FILING DATE: 12-MAR-1996
FILING DATE: 12-MAR-1996
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
FILEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LUNFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TUBENCH: 417 amino acide
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Best Local Similarity 100.
Matches 417; Conservative
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CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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Sequence 6, Application US/09993234

Sequence 6, Application US/09993234

GENERAL INCORPORATION:

APPLICANT: Ashkenazi, Avi J.

TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

STREET: 400 Point San Bruno Blvd

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION NUMBER: US/09/993,234
FILING DATE: 19-No. US20020146768A1-2001
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2323; DB 9;
100.0%; Pred. No. 5.3e-163;
ive 0; Mismatches 0;
PRIOR FILING DATE: 1999-05-04

PRIOR PILING DATE: 1998-03-17

PRIOR PILING DATE: 1998-03-17

PRIOR APPLICATION NUMBER: 60/054,021

PRIOR PILING DATE: 1999-7-07-29

PRIOR APPLICATION NUMBER: 60/040,846

PRIOR APPLICATION NUMBER: 60/040,846

PRIOR FILING DATE: 1997-03-17

NUMBER: OF SEQ ID NOS: 14

SEQ ID NO 5
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61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,889
                                                                                                                                                                                                                                                                                                                                                                      NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/815,469
FILING DATE:
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-607-1996
PRICE PRICE TON NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY AGENT INFORMATION:
PC-DOS/MS-DOS
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Gentz, Reiner
Yu, Guo-Liang
Su, Jeffrey
Rosen, Craig A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 417 amino acids TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM:
                                                                                              FILING DATE:
CLASSIFICATION:
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; Publication No. US20030077694A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Dixit, Vishva
APPLICANT: Dillon, Patrick J.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
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                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 2323; DB 9;
100.0%; Pred. No. 5.3e-163;
rative 0; Mismatches 0;
            ATTORNEY AGENT INFORMATION:
NAME: MARSCHANG, Diane L.
RAGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELEPHONE: 415/225-981
TELEX: 910/311-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear; SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-993-234-6
APPLICATION NUMBER: 08/828,683
                                                                                                                                                                                                                                                                                  LENGTH: 417 amino acids
TYPE: Amino Acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 417; Conservative
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         NUMBER OF INVENTION: Death Domain Concaining Receptor 5
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
CITY: Rockville
COUNTY: US
ZIATE: MD
COUNTY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRAATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/005,842
FILING DATE: 07-Dec-2001
CLASSIFICATION ANDATA:
APPLICATION NUMBER: US/10/005,842
FILING DATE: 07-Dec-2001
CLASSIFICATION ADATA: ADALOGATION ANDATA
TITLE OF INVENTION: Death Domain Containing Receptor
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/042,583
FILING DATE: «Unknown»
APPLICATION NUMBER: US 60/040,846
FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: HOOVER, KENLEY
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLGCY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3013098504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELEFAX: 3013098439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-005-842-5
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CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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Sequence 6, Application US/10081280
Publication No. US20020165157A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/081,280

FILING DATE: 21-Feb-2002

CLASSIFFCATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 2323; DB 13; 100.0%; Pred. No. 5.3e-163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270
FILING DATE: 31.Mar-1997
ATTORNEY/AGENT INFORMATION:
NAME: MARESCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION TELEPHONE: 415/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 417 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELERAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                  STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 417; Conservative
                                                                                                                                                                                                                                                                              COUNTRY: USA
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CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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     301 DQLPSRALGPAAAPTLSPESPAGSPAMILQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
                                      301 DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240
                                                                                                         361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGF 417
                                                                                                                                     121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRIT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,193
FILING DATE: 28-Mar-2002
CLASSIFCATION OF ADMINOWN-PLICATION NUMBER: 08/928,069
FILING DATE: 11-Sep-1997
APPLICATION NUMBER: 60/026943
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 2323; DB 14;
100.0%; Pred. No. 5.3e-163;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                       US-10-112-193-10
Sequence 10, Application US/10112193
Sequence 10, TITLE OF INVENTION: App-3 POLYPEPTIDE 1, NUMBER OF ERQUENCES: 15
SCREESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc. STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAWE: Marechang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 417 amino acids
TYPE: Amino Acid
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Best Local Similarity 100.
Matches 417; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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  361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGF 417
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                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: Winpatin (Genentech)
COMPUTER: Winpatin (Genentech)
COMPUTER: 28-Mar-2002
FILING DATE: 28-Mar-2002
CIASSIFTCATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
FILING DATE: 31-Mar-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 3-3-S-9-1996
APPLICATION NUMBER: 08/710802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence description: seq id no: 6:
US-10-112-793-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 417 amino acids
TYPE: Amino Acid
                                                                                                 US-10-112-793-6; Sequence 6, Application US/10112793; Publication No. US20020192729A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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Best Local (
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CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                  361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGF 417
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                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Wi, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Gentz, Reiner L.
APPLICANT: Gentz, Reiner L.
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Death Domain Containing Receptors
FILE REFERENCE: 1886.031000C
CURRENY APPLICATION NUMBER: US 60/314,314
PRIOR PELICATION NUMBER: US 60/334,134
PRIOR PLING DATE: 2001-09-24
PRIOR PLING DATE: 2000-04-21
PRIOR PAPLICATION NUMBER: US 60/136,741
PRIOR PLING DATE: 1999-05-28
PRIOR PELING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: US 60/136,741
PRIOR PELING DATE: 1999-05-06
PRIOR PELING DATE: 1999-05-06
PRIOR PELING DATE: 1997-03-11
PRIOR PELING DATE: 1997-03-11
PRIOR PELING DATE: 1996-10-17
PRIOR PELING DATE: 1996-10-17
PRIOR PELING DATE: 1996-03-12
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 2323; DB 14;
100.0%; Pred. No. 5.3e-163;
. Mismatches 0;
                                                                                                         ; Sequence 4, Application US/10189189; Publication No. US20030170203A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 417; Conservative
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ORGANISM: Homo sapiens
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                                                                          CTEPCGNSTCLVCPQDTFLAMENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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                                                                                                                        361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERWGLDGCVEDLRSRLQRGP 417
                                                                                                                                        1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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                                                                                                                                                                                                                                                                        Sequence 5, Application US/10175902
Publication No. US20030108516A1
GENERAL INFORMATION:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
FILE REPRENCE: P2931R1C1
CURRENT APPLICATION NUMBER: US/10/211,884
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: 60/02693
PRIOR APPLICATION NUMBER: 60/02693
PRIOR FILING DATE: 1996-09-03
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-10-10
PRIOR FILING DATE: 1997-10-10
PRIOR FILING DATE: 1997-10-10
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-11-24
                                                                                                                                                                                                            301 DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE 360
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                                                                                                         241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
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100.0%; Score 2323; DB 14;
Best Local Similarity 100.0%; Pred. No. 5.3e-163;
Matches 417; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24, Application US/10211884 Publication No. US20030175900A1 GENERAL INFORMATION:
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Watanabe, Colin K.
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Smith, Victoria
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Marsters, Scot A.
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ORGANISM: Homo sapiens
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APPLICANT: Stone, Donna M.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR FILE REFERENCE: P2931R1C1
FILE REFERENCE: P2931R1C1
CURRENT APPLICATION NUMBER: US/10/210,951
CURRENT APPLICATION NUMBER: 60/026943
FRIOR APPLICATION NUMBER: 60/026943
FRIOR APPLICATION NUMBER: 60/059121
FRIOR APPLICATION NUMBER: 60/059121
FRIOR PILING DATE: 1997-07-17
FRIOR FILING DATE: 1997-07-17
FRIOR FILING DATE: 1997-00-19
FRIOR PILING DATE: 1997-10-10
FRIOR APPLICATION NUMBER: 60/062037
FRIOR PILING DATE: 1997-10-17
FRIOR FILING DATE: 1997-10-17
FRIOR FILING DATE: 1997-10-24
FRIOR FILING DATE: 1997-11-24
FRIOR FILING DATE: 1997-11-24
FRIOR PILING DATE: 1997-11-24
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361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP
                                                      361 IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALBRMGLDGCVEDLRSRLQRGP
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                                                                                                                                                                                                                                         Sequence 24, Application US/10210951
Publication No. US20030170228A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pan, James
Pitti, Robert M.
Roy, Margaret Ann
Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                            Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Best Local Similarity 100.
Matches 417; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stone, Donna M.
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US-10-210-951-24
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1 MEORPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLK 1 MEORPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLK 1 MEORPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLK 6 1 CTEPCGNSTCLVCPQDTFLAMENHHNSECARCQACDEQASQVALENCSAVADTRCGCK 1 1 WFVECQVSQCVSSSPPYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVS 1 1 WFVECQVSQCVSSSPPYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVS 1 1 WFVECQVSQCVSSSPPYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVS 1 1 WFVECQVSQCVSSSPPYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVS 1 1 TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADE 1 1 TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADE 2 1 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTW 2 1 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTW 2 1 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTW 2 1 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTW 2 1 MEALTPPRATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTW 3 1 DQLFSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLRE 3 1 DQLFSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLRE 3 1 DQLFSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLRE 3 1 DQLFSRALGBAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLRE 3 1 DQLFSRALGBAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLRE 3 1 DQLFSRALGBAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLRE 3 1 DQLFSRALGBRAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLRE	RESULT 14 SESULT 14 GENERAL INFORMATION: SEQUENCE 24, Application US/10211858 SEQUENCE 24, Application US/10211858 SEQUENCE 24, Application US/10211858 Publication No. USZ003011096A1 SEQUENCE 24, Application US/10211858 Publication No. USZ003011096A1 APPLICANT: Goldowski, Paul J. PRIOR APPLICANTION NUMBER: 60/063045 PRIOR APPLICANTION NUMBER: 60/063045 PRIOR PAUL GOLDOWSKE: 1997-10-21 PRIOR PAUL GOLDOWSKE:	ជα
GY 61 CTEPCGNSTCLVCPQDTPLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120 61 CTEPCGNSTCLVCPQDTPLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120 61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120 CY 121 WFVECQVSGCVSSSPFYCQPCLDCGALHRHTRLLCSREDTDCGTCLPGFYEHGDGCVSCP 180 121 WFVECQVSGCVSSSPFYCQPCLDCGALHRHTRLLCSREDTDCGTCLPGFYEHGDGCVSCP 180 CY 181 TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240 CY 181 TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240 CY 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300 CY 242 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300 CY	RESULT 13 195-10-793-4 196-10-793-4	Query Match 100.0%; Score 2323; DB 14; Length 417; Best Local Similarity 100.0%; Pred. No. 5.3e-163; Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: June 27, 2005, 13:56:23
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JAPPLICANTION: diagnostic method, pathogenicity judging method and
JAPPLICANTION: diagnostic method and medicine of
JAPPLE OF INVENTION: arthritis, and therapeutic method and medicine of
JAPPLE OF INVENTION: chronic rheumatoid arthritis

FILE REFERENCE: TLOP1-2

CURRENT PILIMG DATE: 2003-04-24

PRIOR PILING DATE: 2001-02-4

PRIOR FILING DATE: 2001-3-27

PRIOR FILING DATE: 2001-3-27

PRIOR FILING DATE: 2001-3-27

PRIOR FILING DATE: 2001-3-30

NUMBER OF SEQ ID NOS: 21

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                                                                                                                                                                  1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
                                                                                                                                                                                               1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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                                                                                              Query Match 100.0%; Score 2323; DB 15; Length 417; Best Local Similarity 100.0%; Pred. No. 5.3e-163; Matches 417; Conservative 0; Mismatches 0; Indels 0;
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Matches 417; Conservative
                               TYPE: PRT
ORGANISM: Homo sapiens
US-10-211-858-24
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TYPE: PRT
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SEQ ID NO 24
LENGTH: 41
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MEQRPRGCAAVAAALLLVILGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP

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WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                            TSTLGSCPERCAAVCGWRQMFWVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTADEAG 240
                                                                                                                                                                                                 MEALTPPPATHLSPLDSAHTLIAPDSSEKICTVQLVGNSWTPGYPETQEALCPQVTWSW 300
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1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP 60
                                                                                                                                                                                                                                                                                                                                                                                          IEAVEVEIGRPRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGCVEDLRSRLQRGP 417
                                     CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG
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THIS PACE OLAMA (USO-TO)

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2005
           Copyright
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- protein search, using sw model OM protein Run on:

June 27, 2005, 13:52:39 ; Search time 43 Seconds (without alignments) 436.332 Million cell updates/sec

US-10-081-280-6_COPY_1_195

1 MEQRPRGCAAVAAALLLVLL........CVSCPTSTLGSCPERCAAVC 195 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

99046

283416 segs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 195 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ription	ultra-high-sulfur	high-cysteine chor	high-sulfur kerati	ultra high-sulfur	high cysteine chor	trophozoite surfac	Fas-Delta-(4,7) pr	metallothionein-2	ultra-high-sulfur	finger protein zfo	cysteine-rich hair	protein B0238.12 [zinc finger protei	cellular nucleic a	keratin KAP5.4 - s	ferredoxin-type pr		high sulfur protei	hypothetical prote	hair keratin cyste	finger protein (cl	cellular nucleic a	cellular nucleic a	cellular nucleic a	keratin high-sulfu	high-sulfur wool m	hypothetical prote	•	hypothetical prote
SUMMARIES		! !																												
SUMM	_C	A45910	A23219	837649	S18946	B21761	PC1294	S 58662	S50911	A36686	S70007	I46489	H89044	A55499	148297	146412	AG0369	148298	JC6547	T20467	S60314	806570	A32760	JC2512	I49259	KRGT3M	147108	T24272	KRSH3A	T15651
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	g.	186	178	175	169	143	141	149	104	182	183	126	166	170	170	191	167	171	188	133	151	168	177	177	178	131	152	164	130	188
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	cor	111	107	103.5	103	97	96.5	96	94.5	94	94	90	Q,	89.5	σ	89.5	88	88	88	98	98	84.5	84.5	84.5	84	۳.	83.5	ä	82	81.5
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A,Introns: 17/3 C,Superfamily: chorion class A protein pc292

agglutinin isolect	hypothetical prote	Putative electron	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	iron-sulfur cluste	high-sulfur kerati	hypothetical prote	epithelial cell gl	arginine-vasotocin	probable iron-sulp	probable metalloth	keratin high-sulfu	high-sulfur wool m
A28401	F65072	G65156	T25185	T15610	F86032	H91185	B82430	837650	T20463	D37057	S14480	AB0361	E833.78	KRSHHC	147111
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186	163	157	160	135	157	157	168	177	132	92	161	189	79	152	152
7.2	7.1	7.1	7.1	7.0	7.0	7.0	7.0	7.0	7.0	6.9	6.9	6.9	6.9	6.9	6.9
_	80.5 7.1	80 7.1	80 7.1			79.5 7.0			79 7.0		78.5 6.9		78 6.9		78 6.9

ALIGNMENTS

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Atachigh-sulfur keratin - mouse
Ultra-high-sulfur keratin - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A45910
B;McNab A.R.; Wood, L.; Theriault, N.; Gierman, T.; Vogeli, G.
J; Invest. Dermatol. 92, 263-266, 1989
A;Title: An ultra-high sulfur keratin gene is expressed specifically during hair growth.
A;Title: An ultra-high sulfur keratin gene is expressed specifically during hair growth.
A;Accession: A45910
A;Accession: A5910
A;Accession: A5910
A;Accession A5910
A;Status: preliminary
A;Molecule type: DNA
A;Gestidue: 1-186 <-MCN>
A;Accession: A65910
A;Cross-references: UniPROT: Q64526; GB:M27685; NID:g341749; PIDN:AAA81560.1; PID:g1066818
C;Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A23219
high-cysteine chorion protein B 13 - silkworm
Cippecies: Bembyx mori (silkworm)
Cippecies: Bembyx mori (silkworm)
Cippecies: Bembyx mori (silkworm)
Cipate: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 09-Jul-2004
Cipate: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 09-Jul-2004
Cipate: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 09-Jul-2004
Cipate: 22-Jul-1987 #sequence_recailer in its constant in a chorion multigene family created by tandem duplications and a put A; Reference number: A92960; MUID:85083111; PMID:6439880
A; Reference number: A92960; MUID:85083111; PMID:6439880
A; Residues: 1-178 < ROD>
A; Residues: 1-178 < ROD>
A; Residues: 1-178 < ROD>
A; Cross-references: UNIPROT:P20730
A; Note: the authors translated the codon CTG for residue 48 as Val and GAG for residue 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 Q--VALENCSAVADTRCGCKPGWFVECOVSOCVSSSPFYCQPCLDCGALHRHTRLLCSRR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 OPRCCISSC----CQPC----CRPSCCQSSC---CRPCCQPFCLNLCCQPACSGP 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 CCRICEQPCCVSSCCRIPCCQPCCCVSSCCQPSCCC-----QSSCCQPRCCESSCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 186;
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24.8%; Pred. No. 0.18;
tive 15; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 DIDCGICLPGFYEHGDGCVSCPISILGSCPERCAAVC 195
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Best Local Similarity 24.8%
Matches 39; Conservative
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37 GCGCGCCENFRVCSNSAAPTGLSICSENRYKGDVC---VCGEVPFLGTADVCGNMCSSGC
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F;118-126/Region: Ser-rich nonapeptide repeat
F;127-136/Region: Cys-rich decapeptide repeat
F;137-145/Region: Cys-rich nonapeptide repeat
F;146-155/Region: Cys-rich decapeptide repeat
F;156-165/Region: Cys-rich decapeptide repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-13 < LAT>
C;Superfamily: chorion class A protein pc292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;98-107/Region: Cys-rich decapeptide repeat
                                                                                                                                                                                                                                                                                 A,Map position: 11q13-11q13
C,Superfamily: ultra-high-sulfur keratin
C,Superfamily: ultra-high-sulfur keratin
C,Superfamily: ultra-high-sulfur keratin
F,7-15/Region: Ser-rich nonapeptide repeat
F,59-68/Region: Gly-rich decapeptide repeat
F,79-88/Region: Gy-rich decapeptide repeat
F,79-88/Region: Ser-rich nonapeptide repeat
F,89-97/Region: Ser-rich nonapeptide repeat
                                                                                                                                                                                                                                                                A;Cross-references: GDB:125257; OMIM:148021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 45; Conserv
                                                                                                                          A; Accession: B36686
                                                                                                                                                                                                                                          A; Gene: GDB: KRN1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  high-sulfur keratin - human
Cispecies: Homo sapiens (man)
Cipacies: Homo sapiens (man)
Cipacies: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
Cipacession: 837649
Rizhumabaeva, B.D.; Gening, L.V.; Gazaryan, K.G.
A;Zhumabaeva, B.D.; Gening, L.V.; Gazaryan, K.G.
A;Title: Cloning and structural characterization of human hair sulfur-rich keratin genes
A;Reference number: 837649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-175 <ZHUS
A;Cross-references: UNIPROT:Q07628; EMBL:X63338; NID:g311881; PIDN:CAA44938.1; PID:g3118
C;Superfamily: keratin high-sulfur matrix protein IIIA
                                                   12;
                                                                                                                                                                                       67 NSTCL----VCPQDTFLAWENHHNSECARC-----QACDEQASQ-----VALEN 106
                                                                                                                                                                                                                      : || : || : || : | : |
DRFCLCSNSAAPTGLSICSENRYNGDVCVCGEVPFLGTADVCGDMCSSGCGCIDYGCGDG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECARCQACDEQASQVA---LENCS-AVADTRCGCKPGWFVECQVSQC------ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 -----VSSSPFYCQP----CL-DCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDG 175
                                                                                                                                                                                                                                                                                                                                  -----CGG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCCQTSFCDFLASQLVDLQLSCCQPSCCETSC-CQPSC---CQTSSCGTGCGIGGGIGYG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 QEGSSGAVSTRIRWČRPDCRVEGTČLPPČCVVSCHTPTCČQLHHAEASCČRPSYC--ĞQS 161
                                                                                                                                                                                                                                                                                   CSAVADT -- RCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGT 164
                                                                                                 99
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ultra high-sulfur keratin 1 - human
ultra high-sulfur matrix protein
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Date: Doenecke, D.
S;Drabent, B:; Doenecke, D.
Submitted to the EMBL Data Library, December 1991
A;Reference number: $18946
A;Reference number: $18946
A;Molecule type: mRNA
                                                                                                                       11 VAAALLL----VLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 PRCDCAGDFHKKIGLFCCR-GCPAGHYLKAPCTEP--CGNSTCLVCPQDTFLAWENHHNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161
                                                   72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 175;
9.5%; Score 107; DB 2; Length 178; 23.2%; Pred. No. 0.33; ive 13; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSCSTSG----TCGSSCCOPSC----CETSCCOPSCCETSCC----
                                              77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61; Indels
                                                                                                                                                                                                                                                                                                                               104 CVGITQSCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                              CLPGFYEHGDGCVSCPTSTLGSCPERCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                               ------GCGCGGC-----GGCCGGC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 9.2%; Score 103.5; D
Local Similarity 22.5%; Pred. No. 0.6;
nes 45; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 CVSCPTSTLGSCPERCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- CRPVC 167
                                                49; Conservative
                 Best Local Similarity
Matches 49; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
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    Query Match
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high cysteine chorion B 12 protein precursor - silkworm
high cysteine chorion B 12 protein precursor - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 11-Jan-2000
C;Accession: B21761
R;Iatrou, K.; Tsitilou, S.G.; Kafatos, F.C.
Proc. Natl. Acad. Sci. U.S.A. 81, 4452-4456, 1984
A;Title: DNA sequence transfer between two high-cysteine chorion gene families in the sil
A;Reference number: A21761; MUID:84272653; PMID:6589605
A;Cross-references: UNIPROT:Q14564; EMBL:X63755; NID:g32471; PIDN:CAA45283.1; PID:g32472 R;MacKinnon, P.J.; Powell, B.C.; Rogers, G.E. Cell Biol. 111, 2587-2600, 1990 A;Title: Structure and expression of genes for a class of cysteine-rich proteins of the chiReference number: A36686; MUID:91115951; PMID:1703541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 EQASQVALENCSAVADTRCG-C--KPGWFVECQVSQCVSSSPFYC----QPCLDCGALH 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 PVCCCVPACSCSSCGKRGCGSCGGSKGGCGSCGCSQCSCCKPCCCSSGCGSSCCQCSC-- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CC-GCSGG-----GSSCGGCDSSCGSC-----GSGCRGCGPSCCAPVCCCK 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 CCRGCPAGHYLKAPCTEPCG--NSTCLVCPQDTFLAWENHHNSECARCQ-----ACD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 RHTRLLCSRRDTDCGTCLPGFYEHGDG---CVS-----CPTSTLGS--CPERCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ckpycsockpccsssdrdssccossdrcsscockpccssdcdssccosscockpc 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 VAAALLL----VLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapa
                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-39,'Y',41-169 <MAC>
A;Cross-references: GB:X55293; NID:g34078; PIDN:CAA39005.1; PID:g34079
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 8.6%; Score 97; DB 2; Length 143; I Similarity 21.5%; Pred. No. 1.6; 43; Conservative 14; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.1%; Score 103; DB:
25.3%; Pred. No. 0.63;
tive 6; Mismatches
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116 GCKPGWFVECQVSQCVSSSPF 	Qy 44 GLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDE 97
Oy 176 CVSCPTSTIGSCPERCAAVC 195 CVSCPTSTIGSCPERCAAVC 195 Db 125 CGCCSCGRSC 139	RESULT 8 850911 metallothionein-2 - Tetrahymena pigmentosa C. Snories: Tetrahymena nigmantosa
PC1294 trophozoite surface antigen - Giardia lamblia (strain Adelaide-1) (fragment) C;Species: Giardia lamblia C;Species: Giardia lamblia C;Species: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004 C;Accession: PC1294 R;EY, P.L.; Mayrubcer, G. Gene 129, 257-262, 1993 A;Title: Two genes encoding homologous 70-kDa surface proteins are present within indivi A;Reference number: PC1294; MUID:93314970; PMID:8325510 A;Accession: PC1294 A;Molecule type: DNA A;Residues: 1-141 <exp> A;Rosserences: UNIPROT:P21849; GB:M97488; NID:g159129; PID:g159130</exp>	Cidate: 15-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004 Cidate: 15-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004 Cidate: 15-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004 Cidate: 15-Jul-1995 #sequence_revision in the Ribicolary
	Best Local Similarity 34.3%; Pred. No. 1.9; Matches 23; Conservative 8; Mismatches 29; Indels 7; Gaps 33 CDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSE
Matches 41; Conservative 10; Mismatches 65; Indels 35; Gaps 9; Qy 66 GNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCG 116	Db 40 CTGTGEGCKCTGCKCCQPAKSGCCCGDKAKACCTDPNSGC-CCSSKTNKCCDSTNKTE 96 Qy 89 CARCQAC 95
117 CKPGWFVECQVSQCVSS-SPFYCQPCI	RESULT 9 A36886 ultra-high-sulfur keratin - sheep Cispecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep) Cispecies: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004
DD 111 CLDGYVKSASACTKCDSSCETCNGAALTCKA 141 RESULT 7 S58662 C, Species: Homo sapiens (man) C, Species: Homo sapiens (man) C, Sceries: S8662. S7566	C;Accession: Asbewl, B.C.; Rogers, G.E. R;AacKinnon, P.J.; Powell, B.C.; Rogers, G.E. J. Cell Biol. 111, 2587-2600, 1990 A;Title: Structure and expression of genes for a class of cysteine-rich proteins of the c A;Reference number: A36686, MUID:91115951; PMID:1703541 A;Accession: A36686 A;Status: preliminary A;NDAccule type: DNA A;Regidues: 1-182 cMAC>
Rilli, C.; Cheng, J.; Mountz, J.D. Blochem. J. 310, 957-963, 1995 A)Tille: Differential expression of human Fas mRNA species upon peripheral blood mononuc A,Reference number: S58662; MUID:96013198; PMID:7575433 A,Recession: S58662 A,Status: preliminary; not compared with conceptual translation	A;Cross-references: UNIPROT:P26372; GB:X55294; NID:g1305; PIDN:CAA39006.1; PID:g1306 C;Superfamily: ultra-high-sulfur keratin Cuery Match Best Local Similarity 22.8%; Pred. No. 3; Matches 45; Conservative 6; Mismatches 74; Indels 72; Gaps 13;
•	Qy 7 GCAAVAAALLUVLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTE 63
Submitted for the EMBL Data Library, June 1995 AlReference number: 857565 AlRefertus: preliminary Alrefuns: preliminary Alrefuns: preliminary	QY 64 PCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQYALENCSAVADTRCGCKPGW 121
A;Residues: 1-132 <sch> A;Residues: 1-132 <sch> A;Cross-references: EMBL:X89101; NID:g887457; PID:g887458 C;Keywords: alternative splicing</sch></sch>	OY 122 FVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVS 178
Query Match Best Local Similarity 33.3%; Pred. No. 1.9; Matches 18; Conservative 7; Mismatches 29; Indels 0; Gaps 0;	Qy 179 CPTSTLGSCPERCAAVC 195 Db 130 CGGCGSGCGSSC 141

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protein B0238.12 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: H89044
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/and www_sanger.ac.uk/Projects/C_elegans/A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 24-May.1996 #sequence_revision 24-May-1996 #text_change 24-Sep-1999
C;Accesion: A55499
G;Rocesion: A55499
Genomics 24, 14-19, 1994
A;Telte: Mouse cellular nucleic acid binding proteins: a highly conserved family identifi A;Reterence number: A55499; MUID:95203870; PMID:7896269
A;Reference number: A55499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:016488; GB:chr_V; PIDN:AAB65990.1; PID:g2315490; GSPDB:GN0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 NSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .27 VSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDT--DCG-TCLPGFYEHGDGCVSCPTST 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 GCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 NNVC-QCRSGYV---RNEITRQCVRQAQCS--------RPG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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A,Molecule type: mRNA
A,Residues: 1-170 <RES>
A,Cross-references: GB:L12693; NID:g292347; PIDN:AAA89198.1; PID:g292348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
84 -TCCRPTCCRPGCTRPCCSSGSC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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A;Map position: 3q13.3-3q24
C;Superfamily: cellular nucleic acid-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.9%; Score 89.5; DE Best Local Similarity 23.3%; Pred. No. 6.1; Matches 45; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                zinc finger protein 9 - human
N;Alternate names: nucleic acid binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 -TGFGSSTPFPSQSPQRCG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 LGSCPERCAA-VC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :| :| ||
135 PQACTMQCIVNVC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-166 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: B0238.12
A;Map position: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: GDB: ZNF9
                                  셤
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oysteine-rich hair keratin associated protein - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: 146489; 849201
R;Powell, B.C.; Arthur, J.; Nesci, A.
Bifferentiation 58, 227-232, 1995
A;Title: Characterization of a gene encoding a cysteine-rich keratin associated protein
A;Reference number: 146489; MUID:95228955; PMID:7536172
                                                                                                                                                                                                   C,Accession: S70007 ".o.g. Wilcox, E.R.
R;Rivolta, M.N.; Negrini, C.; Wilcox, E.R.
Biochim. Biophys. Acta 1306, 127-132, 1996
A;Title: A novel zinc finger gene preferentially expressed in the retina and the organ A;Reference number: S70006; WUID:96221281; PMID:8634327
A;Accession: S70007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q15914; EMBL:L41669
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 VCPQDTFLAWENH-----HNSE----CARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 -----FNWSSHLQIHMRVHTGEEPYVCSECGRGFSNSSNLCMHQRVHTGE----- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLC-----SRRDTDCGTCLPGFYEHG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 -------KPFKCE---ECGKAFRHISSLCMHQRVHIGEKPYKCYECGKAFSQRS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 QACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTR 152
                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: mRNA
A;Residues: 1-183 <RIV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 RAQGGTRSPRC-DCAGDF-----HKKIGLFCCRGCPAGHYLKAP--CTEPCGNSTCL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 RDHTGEKVYKCDDCGKDFSTTTKLNRHKKI------HTVEKPYKCYE-CGKA--- 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 CAGDFHKKIGLFCCR-GCPAGHYLKAPCTEP-CGNSTCLVCPQDTFLAWENHHNSECARC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SSCCRP 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .--- 83
                                                                                                                  .nger protein zfOC1 - human (fragment)
Species: Homo sapiens (man)
Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.3%; Score 94; DB 2; Length 183; Best Local Similarity 21.7%; Pred. No. 3; Matches 43; Conservative 16; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.0%; Score 90; DB 2; Length 126; Best Local Similarity 25.4%; Pred. No. 4.7; Matches 43; Conservative 9; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 CGDPCQEES--CCRPSC----CRPQCCQPSCCRPTCCI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-126 <POM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Gene: KAP4L
C,Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 SLČIHQRVHŤ-ĠEKPYŘČ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 DGCVSCPTSTLGSCPERC 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: the ......
C;Keywords: zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
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188 PERCAAVC 195
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                                                                                                                                                                                                                                                                                                                              Cellular nucleic acid binding protein clone 6 - mouse
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cidate: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004
CiAccession: 148297, 819861, 519959
R;Marden, C.H.; Krisans, S.K.; Purcell-Huynh, D.; Leete, L.M.; Daluiski, A.; Diep, A.; T Reformics 24, 14-19, 1994
A;Title: Mouse cellular nucleic acid binding proteins: a highly conserved family identif
A;Reference number: A55499; MUID:95203870; PMID:7896269
A;Accession: 148297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Warden, C.H.
submitted to the EMBL Data Library, January 1992
A;Description: Cellular nucleic acid binding protein (CNBP) is an extremely conserved cy
A;Reference number: S19861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: UNIPROT:P53996; EMBL:Z11870; NID:g50472; PIDN:CAA77896.1; PID:g50473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 CKEPKREREQC----CYNCGKPGHLARDCDHADE-QKCYSCGEFGH--1QKDCTKVKCYR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTEP-----CGNSTCLVCPQDTFLAWENHINSECARCQACDEQASQVALENCSAVADTR 114
                                                                     CTEP-----CGNSTCLVCPQDTFLAWENHINSECARCQACDEQASQVALENCSAVADTR 114
29 MRSRGRGFQFVSSSLPDICYRC-GESGHLAKDCDLQED-----ACYNCGRGGHIAKD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 MRSRGRGFOFVSSSLPDICYRC-GESGHLAKDCDLOED-----ACYNCGRGGHIAKD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X63866; NID:g50470; PIDN:CAA45345.1; PID:g50471
C;Superfamily: cellular nucleic acid-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 170;
                                                                                                                                                                115 CGCKPGWFVECQVSQCVSSSPPYCQPCLDCGALHR 149
                                                                                                                                                                                                || : | | : | | | CG-ETGHV----AINCSKTSEVNCYRCGESGHLAR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG-ETGHV----AINCSKTSEVNCYRCGESGHLAR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 CGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHR 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-191 <JEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 7.9%; Score 89.5; Di
Best Local Similarity 25.2%; Pred. No. 6.2;
Matches 39; Conservative 18; Mismatches
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C,Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 1-170 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-170 <WA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           keratin KAP5.4 - sheep
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                                                                                                                                                                                       63 GCSSCGGSKGSCGSCGG----CGSSCCKPVCCCVPVCSCSSCGKGGCGSSCGGSKGGCG 117
                                                                                                                                                                                                                                                                                                                      ----GCGP----SCCVPVCC 146
                                                                                                                                                                                                                                                                                                                                                                                  132 SSSPFYCOPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGC--VSC--PTSTLGSC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GCSQSSCCRPCCSQSSC 181
                                                                                                                           21 GARAQGGTRSPRCDCAGDFHKKIGLFCCRG-----CPAGHYLKAPCTEPCGNST--CL
                                                               Gaps
                                                               77;
th 7.9%; Score 89.5; DB 2; Length 191; Similarity 22.3%; Pred. No. 6.7; 42; Conservative 8; Mismatches 61; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---CGK--GGCGSC---
                                                                                                                                                                                                                                                                                                                      118 SC-----GGSKGGCGSCGGCGS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                              147 -----CVPACSCSS---
   Query Match
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Search completed: June 27, 2005, 14:02:57 Job time : 44 secs

A BLAM (Body)

cytom cytom cytom cytom

human

human

human human

Q9pzs8 Q8bdc6 Q910h9

cytom

human human

human human human human human

Q68wr4 Q68wx0 Q9pwy0 Q9px31 Q9pzr0 Q9pzr7 Q9pzr7 Q9pzr7

cytom cytom cytom

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63 EPCGNSTCLVCPQDTFLAWENHHNSECARCOACDEQASQVALENCSAVADTRCGCKPGWF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPGLDTDCRECENGTFTASENYLR-QCLSCSKCRKEMYQVEISPCTVYRDTVCGCRKN-- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 VECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- OYRYYWSETHFOCLNCSLC--LNGTVQISCKETONTVCTCHAGFFLRGNECVSC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 VLLALLVEIYPLRVTGLVPHLRDREKRAIPCPQGKYIHPQDNSICCTKCHKGTYLVNDCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAAALLLVLLGARAQG-----GTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A SEQUENCE FROM N.A.

A Duthie S., Nasir L., Eckersall P.D.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

R EMBL; U72244; ABB55089.1; -...
RSP; P19438; IEXT.
GO; GO:0004872; F:receptor activity; IEA.

R InterPro; IPR006209; EGF Tike.
R InterPro; IPR006209; EGF Tike.
R Ffam; PF00020; TNFR, G:
R Pfam; PF00020; TNFR, G:
R PROSITE; PS01196; CYTOCHROME C; UNKNOWN 1.
R PROSITE; PS01166; EGF 2; UNKNOWN 1.
R PROSITE; PS01262; TNFR NGFR 1; 3.
R PROSITE; PS01262; TNFR NGFR 1; 3.
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29.4%; Pred. No. 5.3e-09;
ive 19; Mismatches 90; Indels
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Mammalia, Eutheria, Carnivora, Fissipedia, Felidae,
NCBI_TaxID=9685,
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 26, Last annotation update)
Tumour necrosis factor receptor p60 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189
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Q9PWX3
Q9PZSB
Q8BDC6
Q9DUH9
Q6SWX0
Q9PWY0
Q9PX94
Q9PZR0
Q9PZR1
Q9PZR7
Q9PZR7
Q9PZR7
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1 MEQRPRGCAAVAAALLLVLL......CVSCPTSTLGSCPERCAAVC
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1612378 seqs, 512079187 residues
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O97530
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Maximum Match 100%
Listing first 45 summaries
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Q8SQ52
Q6VZR1
Q9PZS2
Q8SQ49
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Q91IR3
Q9PZS1
Q910W9
Q91IR4
Q9PZR5
Q91IR0
Q6PZR6
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2: uniprot_trembl:*
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Result No.

Sequence:

Run on:

Searched:

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62

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57 LKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCG 116
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Q9ER63; Q87HC0;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
105-JUL-2004 (Rel. 46)
105-JUL-2004 (Rel. 47)
105-JUL-2004 (Rel. 47)
105-JUL-2004 (Rel. 48)
105-JUL-2004 (Rel. 49)
105-JUL-2004 (Rel. 49)
105-JUL-2004 (Rel. 40)
105-JUL-2004 (Rel. 
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STRAIN=129/Sv; TISSUE=Embryonic stem cells;
STRAIN=129/Sv; TISSUE=Embryonic stem cells;
MEDLINE=20519229; PubMed=11063728; DOI=10.1093/hmg/9.18.2691;
Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,
Lane N., Reik W., Walter J.;
"Sequence and functional comparison in the Beckwith-Wiedemann region:
"Sequence and functional imprinting centre and extended imprinting.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=12466268; DOI=10.1074/jbc.M210783200; Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A., Goneider P., Olson D., Tardivel A., Browning B., Lugovskoy A., Goneider D., Dobles M., Hertig S., Hofmann K., Van Vlijmen H., Hsu Y.-M., Burkly L.C., Tschopp J., Zheng T.S., "Identification of a new murine tumor necrosis factor receptor locus that contains two novel murine receptors for tumor necrosis factor-related apoptosis-inducing ligand (TRALL)."; J. Biol. Chem. 278:5444-5454(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND 3D-STRUCTURE MODELING OF 52-160.
STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.3%; Score 173; DB 2; Length 150; 28.9%; Pred. No. 5.5e-07; ive 16; Mismatches 66; Indels ;
GO; GO:0004888; F:transmembrane receptor activity; IEA. GO; GO:0005915; P:apoptosis; IEA. GO; GO:000595; P:immune response; IEA. GO; GO:0007165; P:signal transduction; IEA. InterPro; IPRO08063; Psa receptor. InterPro; IPRO08063; Psa receptor. InterPro; IPRO08063; Psa receptor. PRINTS, PRO0202; TWRR C6; 2. PRINTS; PRO1680; PASRECEPTOR. SWART; SON ROO208; TWRR; 2. PROSITE; PSO5050; TWRR NGFR. 1; UMKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Pan G., Mao W., Risser P.;
"Characterization of SOB, a member of the TNFR family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 AA; 16644 MW; 7DEC76EC40A6BA4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 CKPGWFVECQVSQCVSSSPFYCQPCLDCG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 CKENFY--CNASLC----DHCYHCTSCG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hum. Mol. Genet. 9:2691-2706(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                               Receptor,
NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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             셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 EPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKFG-- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ---WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 RFYW------SETLFQCNNCSLC--LNGTVQISCQEKQNTICTCHAGFFLREHECV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 VLLALLEIYPISVTALVPHPRNRVKRAILCPQGKYIHPQDDSICCTKCHKGTYLYNDCP 73
                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
MEDLINE=21109092; PubMed=11182158; DOI=10.1016/S0165-2427(00)00261-0;
Campbell S.E., Nasir L., Argyle D.J., Gault B.A., Duthie S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 VAAALLLVLLGARAQGGTRSPR-----CDCAGDFHKKIGLFCCRGCPAGHYLKAPCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Gaps
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=Wistar; TISSUE-Corpus luteum;
Lareu R.R., Dharmarajan A.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF104014; AAD20221.1; -.
HSSP; Q92956; lJWA.
GO: 0016020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 189
189 AA; 21324 MW; 5D3AD6A5676BFB99 CRC64;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tumor necrosis factor receptor p60 (Fragment).
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Fas receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning of canine IL-1ra, TWFR and TIMP-2.";
"Cloning of canine IL-1ra, TWFR and TIMP-2.";
EMBL, APO13955, AAD01516.1;
"HSSP, 19438, 1TWR.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR000435; Cytc heme_BS.
InterPro; IPR000435; Cytc heme_BS.
InterPro; IPR000435; Cytc heme_BS.
InterPro; IPR001368; TWFR_GC;
Ffam; PR00209; TWFR_GC; J.
SMART; SM00208; TWFR, 3.
PROSITE; PS01090; CYTOCHROME C; UNKNOWN_1.
PROSITE; PS010186; EGF 2; UNKGONN_1.
PROSITE; PS010186; EGF 2; UNKGONN_1.
PROSITE; PS010180; TWFR_NGFR_1; 3.
PROSITE; PS010652; TWFR_NGFR_1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.4%; Score 197; DB 2; 28.6%; Pred. No. 6.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                             NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 SC 179
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour necrosis family receptor.
                  Mammalia, Eutheria, Prim
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Orthopoxvirus.
NCBL_TaxID=10245;
                                              NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                          Receptor.
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SEQUENCE
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                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed, Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 CCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALEN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 CCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH-DCELCSTCDKDQNMVA--D 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor necrosis factor receptor
superfamily member 23.
Removed in mature form (Potential).
GPI-anchor amidated cysteine (Potential).
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Receptor for the cytotoxic ligand TRAIL. Lacks a cytoplasmic death domain and hence is not capable of inducing apoptosis. May protect cells against TRAIL mediated apoptosis through ligand competition. Cannot induce the NF-kappa-B pathway.
-!- SUBCELLUIAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- TISSUE SPECIFICITY: Ubiquitous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 ANC. 1 (Potential).
14) By similarity.
15 By similarity.
16 By similarity.
16 By similarity.
114 By similarity.
115 By similarity.
147 By similarity.
158 By similarity.
159 By similarity.
160 By similarity.
170 By similarity.
181 By similarity.
182 By similarity.
184 By similarity.
185 By similarity.
186 By similarity.
187 By similarity.
188 By similarity.
189 By similarity.
19594 MW, EE30D617F49DDB7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00652; TNPR NGFR 1; 3.
PROSITE; PS00650; TNPR NGFR 2; 2.
Glycoprotein; GPI-annohr; Lipoprotein; Receptor; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                     EMBL; AJ278264; CAC16405.1; -.
EMBL; AJ276505; CAC27352.1; -.
EMBL; AY165505; AAN87805.1; -.
EMBL; AY165505; AAN87805.1; -.
EMBL; AY165505; AAN87805.1; -.
HSSP; Q92956; LUAA.
HSSP; Q92956; LUAA.
HSSP; Q92956; LUAA.
GO; GO:0005315; F:protein binding; IPI.
GO; GO:0005015; F:protein binding; IPI.
GO; GO:000501; F:tumor necrosis factor receptor activity; IDA.
Film: PF00020; TNFR c6; 3.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.6%; Score 164.5; DB 1; Length 176; 33.7%; Pred. No. 3.2e-06; ative 15; Mismatches 41; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 CSAVADTRCGCKPGWFVECQVSQCVSSSPFYCOPCLDC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 CSATSDRKCECQIGLY-----YYDPKFPESCRPCTKC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Fas receptor CD95 (Fragment).
Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNFR-Cys 1.
TNFR-Cys 2.
TNFR-Cys 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Best Local S
Matches 33
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44 GLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVA 103
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"Vaccinia virus encedes a soluble and cell surface tumour necrosis
"Vaccinia virus encedes a soluble and cell surface tumour necrosis
tfactor receptor that contributes to viral virulence.";
Virology 292:285-298(2002).

R MSSP, 092956; JuMA.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:00060215; P:apportosis; IEA.

R GO; GO:0006955; P:immune receptor activity; IEA.

R GO; GO:0006955; P:immune response; IEA.

R GO; GO:0007165; P:signal transduction; IEA.

R Pfam; PF00020; TURE C6; 2.

R PRINTS; RR01680; PASRECEPTOR.

R SMART; SM00208; TURE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 GOPCRNPCPPGERKARDCTVNEDEPDCVPCQEGKEYTDKGHFSSKCRRCKLCDEGHGLEV
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Vaccinia virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
SEQUENCE FROM N.A.
Petit F., Arnoult D., Lelievre J.-D., Lecossier D., Hance A.J.,
Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=USSR;
MEDLINE=21874859; PubMed=11878931; DOI=10.1006/viro.2001.1236;
                                                                                                         Strange of the EMBL/GenBank/DDBJ databases.

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AF530075, AAM95635.1, -.

EMBL, AF530075, Cimembrane, IEA.

GO; GO:0016020; C:membrane, IEA.

GO; GO:0006918; F:apoptosis; IEA.

GO; GO:0006915; P:apoptosis; IEA.

GO; GO:0006915; P:apoptosis; IEA.

GO; GO:0006915; P:apoptosis; IEA.

GO; GO:0006915; P:apoptosis; IEA.

GO; GO:0006916; P:apoptosis; IEA.

GO; GO:0006916; P:apoptosis; IEA.

GO; GO:0006916; P:apoptosis; IEA.

GO: GO:0006916; P:apoptosis; IEA.

GO: GO:0006916; P:apoptosis; IEA.

InterPro; IPR001368; INFR_C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 14.3%; Score 161.5; DB 2; Length Local Similarity 31.7%; Pred. No. 4.5e-06; les 32; Conservative 12; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 EINCTRIQNIKCRCKFNFF-----CNSAVCEHCDPCTKC 115
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00020; TWFR_c6; 2.
PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TWFR; 2.
PROSITE; PS00652; TWFR NGFR 1; UNKNOWN_1.
PROSITE; PS50050; TWFR_NGFR_2; 2.
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13.7%; Score 155; DB 2;
23.9%; Pred. No. 2.1e-05;
cive 20; Mismatches 62;
                                                                                                                                                                                                                                    186 AA
   153 LLCSRRDTDCGTCLPGFYEHGDG-CVSC 179
                                                         136 --IPKRRCPCG-YFGGIDEQGNPICKSC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPRO01348; TWRR c6.
Ffai. PF00020; TWFR c6; 2.
SMART; SM00208; TWFR; 2.
PROSITE; PS00652; TWFR MGFR 1; UNKNOWN_2.
PROSITE; PS00652; TWFR MGFR 2; 2.
SEQUENCE 186 AA; Z0482 WW; D2342F1040
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                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                           01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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NCBI_TaxID=10243;
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                                                                                                                                                                                                                                                                                                                                       33 CDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARC 92
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                                                                                                                                                                                                                                                                                              33 CDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARC 92
                                                                                                                                                                                                                                 25; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaccinia virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99226947; PubMed=10211965;
Alcani A., Khanna A., Pauli N., Smith J.L.,;
Alcani a virus strains Lister. USSR and Evans express soluble and
cell-surface tumour necrosis factor receptors.";
J. Gen. Virol. 80:949-959(1999).
EMBL; Y17728; CAB41042.1; -.
                                                                                                                                                            Query Match 13.9%; Score 157.5; DB 2; Length 186; Best Local Similarity 28.4%; Pred. No. 1.3e-05; Matches 42; Conservative 17; Mismatches 64; Indels 25.
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GO; GO:0004888; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptoais; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0007165; P:ignal transduction; IEA.
InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; TNFR_G6.
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                                                                                               20662 MW; EF73D6A336A70C5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tumour necrosis factor receptor precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --IPKRRCPCG-YFGGIDEQGNPICKSC 160
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PROSITE; PS50050; TNFR NGFR 2; 2.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
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PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 2.
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                                                                                                  186 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42; Gaps
                                                                                                                                  Cowpox virus (CPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=GRI-90;
MEDLINE=58229462; PubMed=9568042; DOI=10.1006/viro.1998.9039;
Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
"Species specific differences in genome organization of cowpox, smallpox, and vaccinia viruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shchelkunov S.N., Safronov P.F., Totmenin A.V., Miheev M.V., Ryazankina O.I., Petrov N.A., Gutorov V.V., Kotwal G.J., Sandakhchiev L.S.; Sundakhchiev L.S.; Submitted (MRR-2003) to the EMBL/GenBank/DDBJ databases. EMBL; X94355; CAD90723.1; -.
                                                                                                                                                                                                                                                                                                                                                                                         Safronov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V., Shchelkunov S.N., Sandakhchiev L.S., "Genes of a circle of hosts for the cowpox virus."; Dokl. Akad. Nauk 349:829-833(1996).
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Last sequence update)
Last annotation update)
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48 CRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQA-CDEQASQVALEN 106
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            94 RKCPTGSFDKV--KCTGTQNSKCSCLPGWF-----CATDSS-KTEDCRDC----- 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-22760275; PubMed-12878204; DOI=10.1016/S0006-291X(03)01304-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ediplam J.T., Johnson A.L.;
Endagham J.T., Johnson A.L.;
Endagham J.T., Johnson A.L.;
and osteoprotegerin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.0%; Score 146.5; DB 2; Length 146; 28.3%; Pred. No. 9e-05; ive 13; Mismatches 49; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 AA; 16487 MW; 1C9E64FE3A0FC2DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUNA-2004 (TrEMBLrel. 26, Last annotation update)
CD40 protein (Fragment).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and osteoprotegerin.";
Biochem. Biophys. Res. Commun. 307:956-961(2003).
BMBL; Av251407; App03890.1; -.
HSSP; O14763; 1D4V.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR006269; EGF like.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR c6; 2.
SMART; SM00208; TNFR; 3.
                                                                       153 LLCSRRDTDCGTCLPGFYEHGDG-CVSC 179
                                                                                                                              136 --IPKRKCPCG-YFGGIDELGNPLCKSC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-Wistar; TISSUE-Smooth muscle;
                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00208; TNFR; 3.
PROSITE; PS01186; BGF.2; UNKNOWN 1.
PROSITE; PS00652; TNFR NGFR 1; 1.
PROSITE; PS50050; TNFR NGFR 2; 2.
                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 CTSTODRVČECIEGWYLELEF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 GVAQPGTPESDTVCFCCP 146
                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Osteoprotegerin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 28.3 tes 39, Conservative
                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9JKEO;
                                                                                                                                                                                                                                                                                       Q722Y4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9JKE0
                                                                                                                                                                                                                         RESULT 10
Q7ZZY4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                          STAR BERRY REPORTED TO THE STAR A STAR BERRY BER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Brighton Red;
MEDLINE=94378510; PubMed=8091665;
Hu F.Q., Smith C.A., Pickup D.J.;
"Cowpox virus contains two copies of an early gene encoding a soluble
secreted form of the type II TNF receptor.";
Virology 204:343-356(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 CDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAMENHHNSECARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Brighton Red.
STRAIN=Brighton Red.
FUC., Pickup D.J.;
Hu F.Q., Pickup D.J.;
Transcription of the terminal loop region of vaccinia virus DNA is initiated from the telomere sequences directing DNA resolution.";
Virology 181:716-720(1991).
                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Brighton Red;
MEDLINE=83117629; PubMed=6961398;
MEDLINE=83107629; PubMed=6961398;
MEDLINE=83107629; PubMed=6961398;
"Sequence of terminal regions of cowpox virus DNA: arrangement of repeated and unique sequence elements.";
Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parsons B.L., Pickup D.J., "Transcription of orthopoxvirus telomeres at late times during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.6%; Score 153.5; DB 2; Length 186; 28.4%; Pred. No. 2.8e-05; Live 18; Mismatches 63; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dietrich F.S., Ray C.A., Sharma D.A., Allen A., Pickup D.J., Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. EMBL, U55052; AAM13052.1; -.. EMBL, AF482758; AAM13631.1; -..
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Brighton Redgene;
Smith C.A. Goodwin R.G., Pickup D.J.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 AA; 20372 MW; FC720DA743F62A2A CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Soluble TNF receptor CrmC (CrmC or CPXV191 protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; Q92956; 1JMA.

GO; GO:0004872; P:receptor activity; IEA.
Interpro; IPR001368; TNFR.c6.
Pfam; PF00020; TNFR.c6; 2.
PRART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR NGFR.1; UNKNOWN.2.
PROSITE; PS500652; TNFR NGFR.2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 = - ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Brighton Red;
MEDLINE=90177240; PubMed=2309453;
                                                                                                                                 Name=crmC; Synonyms=CrmC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virology 175:69-80(1990).
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STRAIN=Brighton Red;
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Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                        Cowpox virus (CPV)
                                                                                                                                                                                                                                                NCBI_TaxID=10243;
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83 NHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCL 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 SHFSPRCKRCKICDEEHGLEVEKNCTRTQUTKCRCKSNFF--CNVSQC----DHCNPCM 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
"Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
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                                                                                                                                                                                                                                                                                                                                                                          11.8%; Score 133.5; DB 2; Length 124; 29.4%; Pred. No. 0.00096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,0011;
.aa 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 DCGALHRHTRLLCSRRDTDCGTCLPGFYEHG--DGCVSCPTS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 DCGALHRHTRLLCSRRDTDCGTCLPGFYEHG--DGCVSCPTS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016020; C:membrane; IEA.
GO; GO:0004888; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:000055; P:immune response; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; TNFR_C6.
GO:0004888; F:transmembrane receptor activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -------EHGILENCT--PTS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 AA; 16751 MW; 0E192AC4DCE1001F CRC64;
                                                                                                                                                                                                                                                                                                                            124 AA; 14319 MW; 15A7DFF058D79942 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                  GO, GO:0006915; P:apoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:000715; P:signal transduction; IEA.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
PRINTS; PR01640; PASRECEPTOR.
SMART; SM00208; TNFR, 2.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.8%; Score 133.5;
29.4%; Pred. No. 0.00
:ive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSO0652; TNFR NGFR 1; UNKNOWN 1.
PROSITE; PSS0050; TNFR NGFR 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bur. J. Immunogenet. 31:159-166(2004).
EMBL; AB072009; BAB86798.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fas (Fragment).
Felis silvestris catus (Cat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF00020; TNFR c6; 2.
PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 2.
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Q8SQ52;
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                              30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 MC
                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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NON TER
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 CGNSTCLVCPQDTFLAWENHHNSE--CARCQACD-EQASQVALENCSAVADTRCGCKPGW 121
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MEDLINE=99330195; PubMed=10403401; DOI=10.1016/S0014-5793(99)00683-3;
                    Krzesz R., Wagner A.H., Cattaruzza M., Hecker M.;
"Cytokine-inducible CD40 gene expression in vascular smooth muscle
cells is mediated by nuclear factor kappaB and signal transducer and
activator of transcription-1.";
FEBS Lett. 453:191-196(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 FVECQVSQCVSSSPFYCQPCLD --- CGALHRHTRLLCSRRDTDCGTCLPGFYEHG 173
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Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;

"Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
cells.";

Bur. J. Immunogenet. 31:159-166(2004).

EMBL; AB072010; BAB86799.1; --
HSSP; O14763; 100G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Fas delta6 (Fragment).
Felis silvestris catus (Cat).
Evkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.2%; Score 137.5; DB 2; Length 169; 29.1%; Pred. No. 0.00058; tive 15; Mismatches 78; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                        GO, GO: 0016020; C: membrane; IEA.
GO, GO: 0016020; C: membrane; IEA.
GO; GO: 0006915; P: papptcoafs; IEA.
GO; GO: 0006915; P: papptcoafs; IEA.
GO; GO: 0006915; P: papptcoafs; IEA.
GO; GO: 0007165; P: signal transduction; IEA.
InterPro; IPR008065; Fai Ecceptor.
InterPro; IPR001865; Ribosomal_S2.
InterPro; IPR001168; Ribosomal_S2.
InterPro; IPR001168; TNFR_G6.
PEmi; PR00160; FASRECEPTOR.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                             STRAIN=Wistar; TISSUE=Smooth muscle;
Krzesz R., Hecker M.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                      STRAIN=Wistar; TISSUE-Smooth muscle;
Gao D., Hecker M.;
Submitted (WAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF241211, AAF43717.2; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON TER 169 169 - SEQUENCE 169 AA; 18525 MW; F199D91EFA224A26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
PROSITE; PS00623; TNPR NGFR_1; 1.
PROSITE; PS50050; TNFR NGFR_2; 3.
NON_TER
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                                                                                                                                                                                        Canarypox virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                            STRAIN=ATCC VR-111;
PubMed=14671117; DOI=10.1128/JVI.78.1.353-366.2004;
Fulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
The genome of canarypox virus.";
J. Virol. 78:353-366(2004).
EMBL, AY318871; AAR83432.1; -.
EMBL, AY318871; AAR83432.1; -.
InterPro; IPR06209; EGF like.
InterPro; IPR001268; TNFR c6.
Pfam; PF00020; TNFR c6; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.7%; Score 132; DB 2; Length 117; llarity 26.0%; Pred. No. 0.0012; Conservative 24; Mismatches 53; Indels
SMART; SM00208; TNFR; 2.
PROSITE; PS01186; EGF 2; UNKNOWN 1.
PROSITE; PS0652; TNFR NGFR 1; UNKNOWN 1.
PROSITE; PS065050; TNFR NGFR 2; 1.
SEQUENCE 117 AA; 13113 MW; 06E99CAB6A41135A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10359;
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Last sequence update)
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                           CNPV086 TNFR-like protein.
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nes 32; Conserv
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                                                                                                                                                                                                                  Avipoxvirus.
NCBI_TaxID=44088;
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               63 MC-
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Title: Perfect score:

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This novel polypeptidede, designated Apo-2 ligand inhibitor (Apo-2LI), can be used to inhibit apoptosis for therapeutic purposes. Its amino acid sequence was deduced from a human thymus cDNA clone (see AAT91179) and is identical to amino acid residues 1-181 of another novel apoptosis polypeptide, Apo-3 (see AAW26709). It may be a soluble, truncated of
                   Wild type
Human INF
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                   Abg71825 Adm28814 Adm28814 Adm28817 BAdm28817 BAdm56895 Adm5689 BAdm5689 BAdm6668 BAdm668 BAdm6668 BAdm6668 BAdm6668 BAdm6668 BAdm6668 BAdm6668 BAdm668 BAdm6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "N-glycosylated"
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AAR25817
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ABU60675
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/label= Sig_peptide
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96US-00710802.
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N-PSDB; AAT91179.
Modified-site
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23-SEP-1996;
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  Aaw26708 Human apo
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Abu08251 Human Apo
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Abu10202 Human Apo
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              the transmembrane and cytoplasmic sequences of Apo-3. Apo-2LI can be produced in host cells using a claimed method. Chimeric polypeptides comprising Apo-2LI fused to a heterologous amino acid sequence, and an Apo-2LI dimer are also claimed. Apo-2LI can be used to inhibit mammalian cell apoptosis in vivo or ex vivo, and in quantitative diagnostic assays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated monoclonal antibody useful for activating or stimulating apoptosis in cancer cells, comprises an antigen binding site which binds to an Apo-2 ligand inhibitor polypeptide or to an Apo-3 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to an isolated monoclonal antibody comprising an antigen binding site which binds to an Apo-2 ligand inhibitor (Apo-2LI) polypeptide. The antibody of the invention may have cytostatic activity and may act as an activator or simulator of apoptosis in cancer cells, as a blocker of excessive apoptosis or of the autoimmune/inflammatory effects of Apo-3 resulting from nuclear factor (NF)-kappaB activation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APO-2LI; human; apoptosis; monoclonal antibody; Apo-2 ligand inhibitor; cytostatic; cancer; autoimmune; inflammatory; neurodegenerative disease.
                                                                                                                                                                                                                                                      1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLPCCRGCPAGHYLKAP
                                                                                                                                                                                                                             1 MEORPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
 extracellular sequence as well
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                                                                                                                                                       93.0%; Score 1051; DB 2; Length 181; 100.0%; Pred. No. 4.8e-72; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human APO-2 ligand inhibitor (Apo2LI) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG73992 standard; protein; 181 AA.
secreted form of Apo-3, lacking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 48pp; English.
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96US-00710802.
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N-PSDB; ABX15839.
                                                                                                                                                                         Similarity
                                                                                                                        Sequence 181 AA;
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C-Jun-amino-terminal kinase (JNK) activation. The anti-Apo-2 ligand inhibitor is useful in therapeutic purposes for activating or stimulating apoptosis in cancer cells and may be used to block excessive apoptosis (for example in neurodegenerative disease), or to block potential autoimmune/inflammatory effects of Apo-3 resulting from nuclear factor (NF)-kappaB activation or C-Jun-amino-terminal kinase (JNK) activation. The antibody may also be used in diagnostic assays for Apo-2LI or Apo-3, e.g. detecting Apo-2LI or Apo-3 expression in specific cells, tissues or serum, or for affinity purification of Apo-2LI or Apo-3 from recombinant cell culture or natural sources. The present sequence represents the human Apo-2 ligand inhibitor protein (Apo2-LI) which was used to generate the antibody of the invention
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                                                                                                                                                                                                                                                                                                                                                          1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                   Length 181;
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                                                                                                                                                                                                                                                                 93.0%; Score 1051; DB 6;
100.0%; Pred. No. 4.8e-72;
iive 0; Mismatches 0;
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Matches 181; Conservative
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N-PSDB; ABX13176.
                                                                                                                                                                                                                                  Sequence 181 AA;
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The invention relates to an new isolated biologically active Apo-2LI or Apo-3 having at least 80 % sequence identity with native sequence Apo-2LI or Apo-3 appearing as ABU08251 and ABU08252. Also included are a confinearic molecule comprising the Apo-2LI fused to a heterologous amino acid sequence; a dimer molecule comprising a first Apo-2LI and a second Apo-2LI, an antibody that binds to Apo-2LI or Apo-3 for to its certracellular domain sequence), an isolated nucleic acid encoding Apo-2LI or Apo-3, a vector comprising the nucleic acid, a host cell comprising the vector, a method of producing Apo-2LI and a non-human (transgenic or Apo-3, a vector comprising the nucleic acid, a host cell comprising the vector, a method of producing Apo-2LI and a non-human (transgenic or knockut) animal that contains cells that express nucleic acid encoding Apo-3 or cells having an altered gene encoding Apo-3. Apo-2LI or Apo-3 or cells having an altered gene encoding Apo-3. Apo-2LI or Apo-3 or cells having an altered gene encoding Apo-2LI or Apo-3 or cells having an altered gene encoding Apo-2LI or Apo-3 or cells having an altered gene encoding Apo-3. Apo-2LI or Apo-3 or cells having an altered gene encoding Apo-3. Apo-2LI or Apo-3 or cells having an altered gene encoding Apo-3 or cells having anyotrophic lateral sclerosis, multiple sclerosis, reinitis pigmentosa, aplastic anamia, cerebellar degeneration, myocardial infarction, reperfusion injury and toxin-induced liver myocardial infarction, reperfusion injury and toxin-induced liver also useful for preparing a composition for treating cancer. The present sequence represents Apo-2LI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTEPCGNSTCLVCPQDTFLAWENHINSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.0%; Score 1051; DB 6; Length 181; 100.0%; Pred. No. 4.8e-72; ive 0; Mismatches 0; Indels (
    preparing a composition for treating cancer,
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                                                                             Claim 4; Fig 1; 45pp; English.
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Matches 181, Conservative
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The invention relates to an Apo-3 polypeptide having an extracellular domain (BCD) sequence and a death domain sequence. The Apo-3 polypeptide command to stimulate or induce apoptotic activity in mammalian cells. Human Apo-3 exhibits similarities to the tumour necrosis factor receptor (TNFR) family of polypeptides. The invention also relates to a chimeric molecule comprising an extracellular domain sequence comprising residues 1-198 of Apo-3 fused to a heterologous maino acid sequence. The CC conditions such as cancer, lugus, and herpes virus infection. Increased levels of apoptosis are associated with diseases such as acquired conditions such as cancer, lugus, and herpes virus infection. Increased levels of apoptosis are associated with diseases such as acquired immunodeficiency syndrome (AIDS), Alzheimer's disease, parkinson's cimenses, amyotrophic lateral sclerosis, multiple sclerosis, retinitis pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial cinearction, stroke, reperfusion injury, and toxin-induced liver disease.

The Apo-3 polypeptide is also useful in non-therapeutic applications such as in quantitative diagnostic assays as a control against which samples containing unknown quantities of Apo-3 may be prepared, in generating antibodies, as standards in assays for Apo-3 in affinity purification containing unknown quantitically to inhibit apoptosis or nuclear factor shaps B (NF-kappa B) induction, or as an immunogen for producing anti-chappa B induction, or as an immunogen for producing anti-chappas. The chappas B induction, or as an immunogen for producing anti-chappa-3 polypeptides. The present sequence represents the human Apo-2 ligand inhibitor protein which comprises amino acid residues in to 181 of the human Apo-3 protein. It is believed that Apo-2 ligand inhibitor protein which compared form of Apo-3 cigand inhibitor protein which expendence represents the human Apo-2 ligand inhibitor protein which cepter and the apole and the Apo-3 polypeptides.
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                                                                                                                                                                                                                                                                                                                                                       Novel isolated Apo-3 polypeptide useful for inducing apoptosis in mammalian cells, for generating antibodies, in affinity purification techniques, and in competitive-type receptor binding assays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.0%; Score 1051; DB 6; 100.0%; Pred. No. 4.8e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 1; 52pp; English
                                                                                                         97US-00928069.
                                                                                                                                                    96US-0026943P.
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                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                          WPI; 2003-173840/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                               N-PSDB; ABX15460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 T 181
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                                                                                                                                                                                                                                             Ashkenazi AJ;
                                                                                                         11-SEP-1997;
                                                                                                                                                      23-SEP-1996;
                  JS6462176-B1
                                                               08-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
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Best Local S
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(first entry)

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ADA49687 standard; protein; 181 AA.
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                                                           ADA49687;
                          ADA49687
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                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides are useful for stimulating or inducing apoptotic activity in mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy rechniques. The Apo-3 chimeric molecules are useful for inhibiting apoptosis, or as immunogens used in generating antibodies. The antagonistic antibodies may be used to block excessive apoptosis, for instance in neurodegenerative disease, or to block potential autoimmune/inflammatory effects of Apo-3 resulting from NP-kappas activation. The nucleic acid sequences are useful as diagnostics for tissue-specific typing, for preparing Apo-3 polypeptides, or for generating transgenic or knockout animals. The transgenic or knockout animals are useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                                                                                                                                   New isolated Apo-3 polypeptides, useful for stimulating or inducing apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo or ex vivo gene therapy techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      developing and screening of therapeutically useful reagents. The present sequence represents the amino acid sequence of human Apo-2 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG
                                                                                                       Human; Apo-2 ligand inhibitor; apoptosis; gene therapy; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                   cancer; neurodegenerative disease; immunosuppresive; tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated Apo-3 polypeptide. The Apo-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.0%; Score 1051; DB 6; Length 181; 100.0%; Pred. No. 4.8e-72; ative 0; Mismatches 0; Indels (
            ABU10202 standard; protein; 181 AA
                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 1; 50pp; English.
                                                                                                                                                                                                                                   96US-0026943P.
97US-00928069.
                                                                                Human Apo-2 ligand inhibitor
                                                                                                                                                                                                             28-MAR-2002; 2002US-00112193
                                                          11-AUG-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 181; Conservative
                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                   2003-438872/41.
                                                                                                                                                                                                                                                                                                                  WPI; 2003-438872/
N-PSDB; ACA61684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 181 AA;
                                                                                                                                                                JS2003004313-A1
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                                                                                                                                                                                                                                                                                            Ashkenazi AJ;
                                                                                                                                                                                                                                    23-SEP-1996;
11-SEP-1997;
                                                                                                                                          Homo sapiens
                                                                                                                                                                                       02-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or Apo-3 polypeptide which induces or stimulates apoptotic activity, useful
                                                          Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; affinity; competitive-type receptor; binding assay; cancer cell; human; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MEGRPRGCAAVAAALLLVILGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93.0%; Score 1051; DB 6;
100.0%; Pred. No. 4.8e-72;
iive 0; Mismatches 0;
Human Apo-2 ligand inhibitor (Apo-2LI)
                                                                                                                                                                                                                                                                                                                                                                                                 96US-00625328.
96US-00710802.
97US-00828683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Fig 1; 53pp; English.
                                                                                                                                                                                                                                                                                                                                          28-MAR-2002; 2002US-00112793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in diagnostic assays.
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N-PSDB; ADA49691.
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Best Local Similarity
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                                                                                                                                                                                                                  US2002192729-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ashkenazi AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-1996;
31-MAR-1997;
                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1996;
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Tumour necrosis factor receptor extracellular domain H23P

(first entry)

22-SEP-2003

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with rheumatoid arthritis. Certain mutations in the gene can be linked to the disease. The sequences can be used to evaluate disease onset and its possibility and to provide therapy and remedies. The present sequence is a protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the human DR3 gene, which is associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEORPRGCAAVAAALLIVILGARAOGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEQRPRGCAAVAAALLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomes, particularly DR3 genomic DNA, participating in rheumatoid arthritis via mutation, useful in evaluating disease onset and its possibility and providing therapy and remedies.
                                                                                                           Human rheumatoid arthritis associated DR3 gene related protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                        Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.0%; Score 1051; DB 5; Length 188; 100.0%; Pred. No. 5e-72; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 72-73; 84pp; Japanese
                           AA017880 standard; protein; 188 AA
                                                                                                                                                                                                                                                               24-OCT-2001; 2001WO-JP009313.
                                                                                                                                                                                                                                                                                        24-OCT-2000; 2000JP-00324296.
27-MAR-2001; 2001JP-00090546.
30-MAR-2001; 2001JP-00099990.
                                                                                22-AUG-2002 (first entry)
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Best Local Similarity 100.
Matches 181; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          Konishi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-417132/44.
N-PSDB; AAL47187.
                                                                                                                                                                                                                                                                                                                                                              (SHIO/) SHIOZAWA S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 188 AA;
                                                                                                                                                                                                          WO200234912-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ť 181
                                                                                                                                                     gene therapy.
                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                        Shiozawa S,
                                                                                                                                                                                                                                    02-MAY-2002
                                                      AA017880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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RESULT 8
ABR62365
ID ABR6
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AC ABR6
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ABR62365 standard; protein; 161 AA.

ABR62365

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This is the protein sequence of a mutated extracellular domain of the p55 tumour necrosis factor receptor (TNFTED) in which a Pro residue substitutes the native His-34 residue (residue 23 in the present sequence) and an Ile residue substitutes the native Ser-57 residue (residue 46 of the present sequence). Screening of TNFTED mutant clones using a yeast display system yielded a clone that showed a higher expression level in yeast than did a wild-type TNFTED clone. The encoded polypeptide contained these 2 amino acid substitutions. The introduction of proline residues may assist the polypeptide to adopt a favourable conformation that fixes the neighbouring cysteine residue into the correct orientation for disulfide bond formation, resulting in a higher invention therefore provides methods of increasing protein expression levels by substituting an amino acid residue with proline, where the substitution occurs within 15 (preferably within 10, and especially within 5) amino acids of a cysteine residue. Note: The present sequence is not shown in the specification but is derived from the TNFTED sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 GQVEISSCTVDRDITVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
                                                                           Numour necrosis factor; receptor; TNFrED; proline; protein engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Increasing expression of a protein, comprises substituting at least one codon in the polynucleotide encoding the protein, for a codon encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 SQVALENCSAVADTRCGCKPGWFVEC---OVSQCVSSSPFYCQPCLDCGALHRHTRLLCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6; Length 161;
                                                                                                                                                                                                            /note= "wild-type His substituted by Pro"
                                                                                                                                                                                                                                           /note= "wild-type Ser substituted by Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 RRDIDCGICLPGFYEHGDGCVSCPISILGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.3%; Score 206.5; DB 6;
30.4%; Pred. No. 4.4e-08;
Micmatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                               (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Schweickhardt RL;
                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page; 53pp; English.
                                                                                                                                                                                                                                                                                                                                             21-NOV-2002; 2002WO-EP013059
                                                                                                                                                                                                                                                                                                                                                                              30-NOV-2001; 2001US-0340648P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Brondyk W, Jiang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-523245/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                              Misc-difference 46
                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 161 AA;
                                                                                                                                                                                                                                                                            WO2003046160-A2
                                                                                              mutant; mutein.
                                                                                                                               sapiens.
                                                                                                                                                                                                                                                                                                              05-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49;
                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proline.
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human tumour necrosis factor (TNP) receptor related protein TR2. Included human tumour necrosis factor (TNP) receptor related protein TR2. Included to the the two splice variants of TR2. TR2-SY1 and TR2-SY2.

The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a conservation of the TNPR superfamily. The invention includes a method for the treatment of arthritis or inflammation using an antibody directed against a fragment of the TNPR superfamily. The invention includes a method for the transportance of the TNPR superfamily. The invention includes a method for the transportance of transportance of the TNPR superfamily. The invention includes a method for the artipodies exhibit cytostatic, dermatological, antianaemic, antializergic, antiathmatic, antializergic, antiathmatic, antianaemic, antializergic, antiathmatic, antianatory, neuroprotective, nootropic, antianaemic, antianiflammatory, neuroprotective, nootropic, antianaemic, antianiflammatory, neuroprotective, antiathmatic, antianiflammatory, neuroprotective, antiathmatory activity. The methods are useful for treating arthritis or immunodeficiency or for enhancing an in vivo leukocyte response to an antigen. Anti-TR2 antibodies are useful for treating, inhibiting or preventing autoimmune diseases (such as autoimmune haemolytic anaemia, dermatitis, allergic encephalomyellitis, rheumatoid arthritis, asthma, and cor morphalomyellitis, theumatoid arthritis, asthma, and inflammatory myopathies) and immunodeficiency disorders (such as severely combined immunodeficiency (SCID) x linked, B coll lymphoproliferative disorder, or Nezelof syndrone-combined immunodeficiency with Igs). TR2-SV2 polymucleotides and polypeptides, agonists or antagonists are useful for treating or preventing autoimmune diseases and inhibit the growth, progression and/or metastasis of cancers. They are also used to activate, differentiate or proliferate cancerous cells or tissues, and can be used to treat diseases associated with increased cell survival, or the inhibition of 
                                                                                                                                                                                                Tumour necrosis factor-receptor related protein; TR2; human; cancer; chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease; immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID; severely combined immunodeficiency; apoptosis inhibition; Alzheimer's disease; Parkinson's disease; Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid molecule encoding a human tumor necrosis factor receptor 2 and its two splice variants, useful for treating arthritis or inflammation, cancer (such as follicular lymphomas) and immunodeficiency
                                                                                                                                                          Tumour necrosis factor receptor (TNFR) domain of TNFR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 16, 373pp, English.
                     AAY94711 standard; protein; 154 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0125683P.
99US-0126522P.
99US-0135169P.
99US-0147383P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAR-2000; 2000WO-US007521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gentz RL;
                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-594519/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NI J.
ROSEN C A.
GENTZ R L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                     WO200056405-A2.
                                                                                                                                                                                                                                                                                                                                             sapiens
                                                                                                              29-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders.
                                                                 AAY94711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NIJJ/)
(ROSE/)
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                                                                                                                                                                                                                                                                                                                                          Homo
AAY9471
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                                                                                                                                                                                                                                                                                              100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                                                                                                                                                                                                                                                                                  68 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or Apo-3 polypeptide which induces or stimulates apoptotic activity, useful in diagnostic assays.
as sources for generating antibodies, as molecular weight markers. This sequence represents the tumour necrosis factor receptor (TNFR) domain of the human TNFR-1 protein. The sequence was used in the characterisation
                                                                                                                                                                                                                   40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                                                                                                                                                                       9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                               Gaps
                                                                                                                                                                               21;
                                                                                                                                         17.7%; Score 200.5; DB 3; Length 154; 29.8%; Pred. No. 1.2e-07; ive 20; Mismatches 72; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apo-2 ligand inhibitor, Apo-2LL; Apo-3; apoptosis; affinity; competitive-type receptor; binding assay; cancer cell; human; TNF receptor family; hTNFR1; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                          157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                 Extracellular region of human TNFR1 (hTNFR1) protein.
                                                              of the TR2 receptor protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA49698 standard; protein; 154 AA
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96US-00710802.
97US-00828683.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                             48; Conservative
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                                                                                                                                           Query Match
Best Local Similarity
                                                                                                    Sequence 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS2002192729-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ashkenazi AJ;
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23-SEP-1996;
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ADA49698
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fragment of the amino acid residues 68-240 of the Human apoptosis
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21-MAR-1997,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-AUG-1999;
02-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local &
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  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibody that binds to human Apoptosis Inducing Molecule II (AIM II) protein, useful for preparing a composition for treating e.g., lymphadenopathy, autoimmune disease, rheumatoid arthritis, osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated antibody or its portion binding to a protein comprising a protein whose sequence comprises an immunogenic
                                                                                                                                                                                                                                     100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                                                                                                                                                                                                                          68 GOVEISSCTVDRDTVCGCRKNQYRHYWSENLFOC----FNCSLCLN-GTVH----LSCQ 117
                                                                                                                                                          66
                                                                                                                                                                                             9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                        40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumour necrosis ligand superfamily, lymphotoxin-beta receptor, TR6, TRAIL receptor 6; lymphadenopathy, aberrant bone development; autoimmune disease, graft-versus-host disease, rheumatoid arthritis;
                                                                                                                 Indels 21;
                                                                                Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human tumour necrosis factor receptor-I cysteine rich motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; apoptosis inducing molecule II; AIM II; antibody;
                                                                                                                                                                                                                                                                                                                 157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                              72;
                                                                                DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhai Y;
                                                                          17.7%; Score 200.5; DB (29.8%; Pred. No. 1.2e-07; ive 20; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 13; SEQ ID NO 53; 163pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADL17741 standard; protein; 154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 osteoarthritis; cancer; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0124041P.
99US-0137457P.
99US-0142657P.
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97US-00822953.
98US-0003886.
98US-00027287.
98US-0075409P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-2004 (first entry)
                                                                                            Local Similarity 29.89 tes 48; Conservative
region of human Apo-2LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-810570/76.
                                       Seguence 154 AA;
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02-DEC-1999;
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04-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADL17741;
                                                                            Query Match
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inducing molecule II, AIM II, appearing as ADL17690 or a procein whose sequence comprises a fragment of amino acid residues 68-240, where the fragment comprises at least lot a so amino acid residues. Also included are a hybridoma that produces the antibody, a method of detecting in a biological sample a protein that binds the antibody or its portion, a composition comprising the antibody and a carrier and an isolated cell that produces the antibody and a carrier and an isolated cell necrosis ligand superfamily and has been shown to bind lymphotoxin-beta receptor and TR6 (TRAIL receptor 6). The antibody is useful for preparing a composition for treating e.g., lymphadenopathy, aberrant bone development, autoimmune disease, graft-versus-host disease, rheumatoid arthritis, osteoarthritis or cancer (many other diseases and conditions are listed in the specification). The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 GOVEISSCTVDRDTVCGCRKNQYRHYWSENLFOC----FNCSLCLN-GTVH----LSCQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS
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idiopathic thrombocytopenic purpura, cellular response;
T-cell activation; molecular weight marker; human; TNF receptor; TNFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apoptosis inducing molecule II; AIM II; TNF; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy; graft versus host disease; immunodeficiency; cancer; autoimmune disease; multiple sclerosis; type I diabetes; rheumatoid arthritis; primary biliary cirrhosis; aplastic anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7; Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 EKQNTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.7%; Score 200.5; DB 7, 29.8%; Pred. No. 1.2e-07; ive 20; Mismatches 72,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADJ56814 standard; protein; 154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human TNFR-I cysteine-rich motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0013923P.
96US-0030157P.
97US-0082853.
98US-00027287.
98US-0027287.
99US-00252656.
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99US-0142657P.
99US-0148326P.
99US-0168380P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003; 2003US-00375680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity 29.8
48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 154 AA;
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New ethylene! glycolated polypeptide(s) with improved pharmacokinetic properties - for treating e.g. TNF and IL-1 mediated diseases, e.g. adult respiratory distress syndrome, rheumatoid arthritis, septic shock etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
                                                                                                                                                                                        This invention describes novel polynucleotide sequences encoding tumour necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP). The products of the invention are useful in pharmaceutical compositions for prophylaxis or treatment of human tumnours and to understand the mechanisms of TNF action. This sequence represents a fragment of the TNF-BP described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                 40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour necrosis factor; ethylene glycol; pharmokinetic; adult respiratory distress syndrome; rheumatoid arthritis; septic shock; pulmonary fibrosis; spacer.
                                                                                                     DNA encoding TNF binding protein and TNF- receptor - used in tumour treatment and to understand mechanisms to TNF action.
                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                Length 161;
                                                                                                                                                                                                                                                                                                                                                                                72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brewer MT, Kohno
                                     Stratowa C;
                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                              17.7%; Score 200.5; DB 29.8%; Pred. No. 1.2e-07; ive 20; Mismatches 72
                                       Maurerfogy I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evans RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR27496 standard; protein; 161 AA.
                                                                                                                                                          Claim 23; Page 34; 51pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91US-00669862.
92US-00822296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Native 30 kD TNF inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                48; Conservative
                                     Himmler A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Armes LG,
   (SYND ) SYNERGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SYND ) SYNERGEN INC
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                     WPI; 1990-321987/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-348933/42.
                                                                                                                                                                                                                                                                                                            Sequence 161 AA;
                                       Hauptmann R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409216221-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rhompson RC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
09-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR27496;
                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                   The invention relates to apoptosis inducing molecule II (AIM II), a TNF (tumour necrosis factor)-ligand superfamily member and its corresponding nucleic acid sequence. The invention is useful for preventing, treating, ameliorating, diagnosing or prognosing graft versus host disease, treating, immunodeficiency, cancer, autoimmune diseases such as multiple sclerosis, type I diabetes, rheumatoid arthritis, primary biliary cirrhosis, aplastic anaemia, myelodysplasia, systemic lupus erythematosus and idiopathic thrombocytopenic purpura. It is useful for screening or identifying compounds capable of enhancing or inhibiting cellular sesponse induced by AIM II, for inhibiting, blocking or reducing T-cell activation. AIM II is useful as a molecular weight marker on SDS-PAGE gels or on gel filtration columns. The present sequence is a cysteinerich motif of human TNF receptor (TNFR) family member.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 GQVEISSCTVDRDTVCGCRKNQYRHYMSENLFQC----FNCSLCLN-GTVH----LSCQ 117
                                                                                                                                                     Isolated apoptosis inducing molecule II polypeptide, useful for treating, preventing, ameliorating, diagnosing or prognosing autoimmune diseases such as multiple sclerosis, rheumatoid arthritis, aplastic anemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 HPONNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INF; human; tumour necrosis factor; tumour necrosis factor receptor; INF-R; tumour necrosis factor binding protein; TNF-BP; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.7%; Score 200.5; DB 8; Length 154; 29.8%; Pred. No. 1.2e-07; ative 20; Mismatches 72; Indels 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 EKONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 153
                                                                                     Ullrich S;
                                                                                                                                                                                                                          Example 13; SEQ ID NO 53; 189pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
                                                                                     Yu G, Ruben SM, Zhai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG74752 standard; protein; 161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human TNF binding protein fragment
10-MAR-2000; 2000US-00523323.
01-MAR-2002; 2002US-0360234P.
                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90EP-00106624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89DE-03920282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89DE-03913101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48; Conservative
                                                                                                                     WPI; 2004-201265/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUN-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP393438-A.
                                                                                     Ebner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG74752;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                           contain at least one non-native cystein residue, pref. at positions 1, 194, 105, 111 and/or 165. The non-native cysteine is joined to a non-peptidic polymer, pref. monomethoxy PGG via thio-ether bonds. Two such TNF inhibitor mols. may be linked via this on-peptidic spacer. The modified polypeptides show improved pharmokinetic properties, i.e. increased mol. wt. hence reduced clearance rate following s.c. or systemic administration, increased sol. of native TNF inhibitors, and reduced antigenicity. The polypeptides may be used for treatment of TNF mediated diseases such as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid arthritis, inflammatory bowel disease and septic shock. The same method may be applied to the interleukin-1 receptor antagonist IL-1ra. See also AAR27495. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                 40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                                                                                                                                                                                                                                                                                                                      11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 69
                               sequence shows a native 30 kD TNF inhibitor which may be modified to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treatment of acute or chronic inflammatory disease, e.g. leukaemia - by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate.
                                                                                                                                                                                                                                                                                                                                                 21; Gaps
                                                                                                                                                                                                                                                                                                              17.7%; Score 200.5; DB 2; Length 161; 29.8%; Pred. No. 1.2e-07; Live 20; Mismatches 72; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; tumour necrosis factor; TNF; TNF receptor type I; inflammatory disease; leukaemia; TNF binding protein; anti-inflammatory drug; methotrexatess.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 EKONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      soluble tumour necrosis factor receptor type I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Edwards CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW59664 standard; protein; 161 AA
Claim 54; Fig 2; 100pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0032587P.
97US-0036355P.
97US-0039315P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sennello RM,
                                                                                                                                                                                                                                                                                                                                                 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-333039/29
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAV41548.
                                                                                                                                                                                                                                                                                  Sequence 161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-DEC-1996;
23-JAN-1997;
07-FEB-1997;
09-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9824463-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUN-1998
                                                                                                                                                                                                                                                   PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
                                                                                  receptor type I, used in the method of the invention involving the treatment of acute or chronic inflammatory disease such as leukaemia by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM
                                                                                                                                                                                                                                                                                                                                                                                                                                40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                            This is the amino acid sequence of the human tumour necrosis factor
                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                       DB 2; Length 161;
                                                                                                                                                                                                                                                                                                 17.7%; Score 200.5; DB 2; Length 3 29.8%; Pred. No. 1.2e-07; ive 20; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: June 27, 2005, 14:02:08
Disclosure; Fig 1; 104pp; English.
                                                                                                                                                                                                                                                                                                    Query Match 17.7
Best Local Similarity 29.8
Matches 48; Conservative
                                                                                                                                                                                                                                           Sequence 161 AA;
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Sequence 430, App Sequence 16, Appl Sequence 10, Appl Sequence 11, Appl Sequence 421, Appl Sequence 21, Appl Sequence 21, Appl Sequence 429, Appl Sequence 429, Appl

Sequence 423, App

Sequence 3, Appli Sequence 4, Appli Sequence 12, Appli Sequence 3, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MinParin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/884,733
FILING DATE: 19-Jun-2001
CLASSIFICATION: UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | US-09-884-733-1
| Sequence 1, Application US/09884733
| Patent No. US20020123116A1
| GENELL INFORMATION:
| APPLICANT: Ashkenazi, Avi J.
| TITLE OF INVENTION: Apo-2 Ligand Inhibitor
| NUMBER OF SEQUENCES: 9
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Genentech, Inc.
| STREET: 460 Point San Bruno Blvd
| CITY: South San Francisco
| STATE: California
14 US-10-218-102-423

14 US-10-218-102-4330

US-09-899-429A-10

US-09-899-429A-10

US-09-899-429A-10

US-09-98-789-11

US-10-218-102-421

US-09-798-789-19

US-09-798-789-19

US-09-798-789-19

US-09-798-789-19

US-09-798-789-19

US-09-798-789-19

US-09-798-789-19

US-09-798-789-19

US-09-798-789-19

US-09-808-12

US-09-808-12

US-09-808-12

US-10-112-793-12

US-10-112-793-12

US-10-989-422-4
                                                                                                                                                                                                                                                                        US-09-899-422-4
US-09-907-253-2
US-09-907-253-2
US-09-899-429A-4
US-09-899-429A-4
US-09-792-356-4
US-09-882-735-2
US-10-436-826-73
US-10-436-826-73
US-10-421-783-2
US-10-496-218-1
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US-10-218-102-424
US-10-218-102-432
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US-09-798-789-14
US-09-798-789-22
US-09-899-429A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFRAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/304,003
FILING DATE: 14-JUNE-2000
ATTORNEY/AGENT INFORMATION:
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   Sequence 5, Appli
Sequence 12, Appl
Sequence 422, App
Sequence 18, Appl
Sequence 13, Appl
Sequence 20, Appl
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Sequence 1, Appli
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1 MEQRPRGCAAVAAALLIVLL.......CVSCPTSTLGSCPERCAAVC 195
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-993-234-1
3 US-10-081-280-1
4 US-10-112-793-1
5 US-10-112-193-1
5 US-10-12-147-5
US-09-798-789-12
US-09-899-4284-18
US-09-798-789-13
US-09-798-789-13
US-09-798-789-13
                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                     1717557 seqs, 384547976 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                             - protein search, using sw model
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Maximum DB seq length: 195
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93.0
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118.5
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Result Š

Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 1, Appli Sequence 9, Appli Sequence 6, Appli

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STATE: California
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                                                                                                                                                                                   93.0%; Score 1051; DB 9; Length 181; 100.0%; Pred. No. 5.8e-76; Live 0; Mismatches 0; Indels (
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Patent No. US20020146768A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: 1
STREET: 460 POINT SAN Bruno Blvd
CITY: South San Francisco
STRATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible OPERATING SYTEM: PC-DS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/993, 234
FILING DATE: 19-No. US20020146768A1-2001
CLASSIFICATION DATA:
APPLICATION DATA:
ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Marschang, Diane L.
REGIGSTATION UNDERS: 35,600
REFFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
                                                                                                                          ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-884-733-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-993-234-1
                   INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 181 amino acids
TYPE: Amino Acid
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                        TOPOLOGY: Linear
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                                                                                                                                                                                               CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                                                                                                                                                                                                                                                            121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
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                                                    Gaps
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     Length 181;
                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10081280
Publication No. US20020165157A1
GENERAL INFORMATION:
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.0%; Score 1051; DB 13; 100.0%; Pred. No. 5.8e-76;
93.0%; Score 1051; DB 9;
100.0%; Pred. No. 5.8e-76;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WinPatin (Generatech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/081,280
FILING DATE: 21-Feb-2002
CLASSIFICATION CURNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,270
FILING DATE: 31-Mar-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: P1007R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Marschang, Diane L. REGISTRATION NUMBER: 35,600
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TELEPHONE: 415/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 181 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415/952-9881
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61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCDACDEQASQVALENCSAVADTRCGCKPG 120
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/112,193 FILING DATE: 28-Mar-2002 CLASSIFICATION: CURknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1051; DB 14;
Pred. No. 5.8e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/928,069
FILING DATE: 11-26P-1997
APPLICATION NUMBER: 60/026943
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORWATION:
NAME: MATSCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                   APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-3 POLYPEPTIDE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                     CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 181 amino acida
TYPE: Amino Acid
                                                                                                                                                                      Sequence 1, Application US/10112193
Publication No. US20030004313A1
GENERAL INFORMATION:
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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US-10-415-247-5
                                                                                                                                                      US-10-112-193-1
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Best Local
                                                                                                                                RESULT 5
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                                                                                       121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
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                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/10112793
Publication No. US20020192729A1
GENERAL INFORMATION:
APPLICANT: CORRESPONDENCE: 28
CORRESPONDENCE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity 100.0%; Score 1051; DB 13; Similarity 100.0%; Pred. No. 5.8e-76; 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-4pr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-112-793-1
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 181; Conservative
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                                                                                                                                                                                                                                                                                         71 GQVEISSCTVDRDTVCGCRKN----QYRHYETENEFFCFNCSLCINGTVH---LSCQE 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 GQVEISSCTVDRDTVCGCRKN----QYRHYETENEFFCFNCSLCLNGTVH----LSCQE 121
                                                                                                                                                           12 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASE-EHKRECLRCSRCRDKM 70
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                                                                                                                       40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

JAPPLICANT: Dahiyat, Bassil I.

APPLICANT: Designaliais, John R.

APPLICANT: Vielmetter, Jost
FILE REFERENCE: A-6722-11/RFT/RMS/RMK

CURRENT APPLICATION PROBER: US/10/218,102

CURRENT FILING DATE: 2002-08-12

PRIOR PILING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2001-09-10

PRIOR PLING DATE: 2001-09-25

PRIOR FILING DATE: 2002-01-25

PRIOR FILING DATE: 2002-01-25

PRIOR PLING DATE: 2002-01-25

PRIOR APPLICATION NUMBER: US 60/352,103

PRIOR PLING DATE: 2002-01-25

PRIOR PLING DATE: 2002-01-25

PRIOR APPLICATION NUMBER: US 60/352,103

PRIOR PLING DATE: 2002-01-25

PRIOR PLING DATE: 2002-01-25
                                                        Gaps
                                                        19;
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                       Best Local Similarity 30.0%; Pred. No. 3.4e-09;
Matches 48; Conservative 20; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73; Indels
                                                                                                                                                                                                                                                                                                                                                                               158 RDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                       122 KONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 156
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30.0%; Pred. No. 3.4e-09;
tive 20; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 422, Application US/10218102
Publication No. US20030130827A1
GENERAL INFORMATION:
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; GENERAL INPORMATION:
APPLICANT: Hauptmann, Rudolph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 5, Application US/10415247

Publication No. US20040013655A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Shiozawa, Shunichi

TITLE OF INVENTION: Genome responsible for chronic rheumatoid arthritis,

TITLE OF INVENTION: diagnostic method, pathogenicity judging method and

TITLE OF INVENTION: arthritis, and therapeutic method and medicine of

TITLE OF INVENTION: arthritis, and therapeutic method and medicine of

TITLE OF INVENTION: chronic rheumatoid arthritis

CURRENT APPLICATION NUMBER: US/10/415,247

CURRENT FILING DATE: 2003-04-24

PRIOR APPLICATION NUMBER: UP 2000-324296

PRIOR PRILING DATE: 2001-30-24

PRIOR FILING DATE: 2001-3-27

PRIOR FILING DATE: 2001-3-27

PRIOR FILING DATE: 2001-3-27

PRIOR FILING DATE: 2001-3-27

NUMBER OF SEQ ID NOS: 21

SSOT UD NOS: 21

SSOT UD NOS: 21
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Fatent No. US2002000978041

GENERAL INFORMATION:

APPLICANT: Dahiyat, Bassil

APPLICANT: Filikov, Anton

TITLE OF INVENTION: DISORDERS

TITLE OF INVENTION: DISORDERS

TITLE OF INVENTION: DISORDERS

TITLE OF INVENTION: DISORDERS

TITLE OF INVENTION: US/09/798,789

CURRENT APPLICATION NUMBER: US/09/798,789

CURRENT FILING DATE: 2001-03-02

FRIOR PILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PATENTIN VOICE: 21
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US-09-798-789-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 93.0%; Score 1051; DB 15; Best Local Similarity 100.0%; Pred. No. 5.9e-76; Matches 181; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-415-247-5
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LENGTH: 162
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GENERAL INFORMATION:
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FEATURE:
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          APPLICANT: Murer-Fogy, Ingrid
APPLICANT: Stratowa, Christian
TITLE OF INVENTION: The Receptors, TNF Binding Proteins and DNAS Coding for
TITLE OF INVENTION: Them
TITLE OF INVENTION: Them
FILE REFERENCE: 98-385-J
CURRENT APPLICATION NUMBER: 08/09/899,429A
CURRENT APPLICATION NUMBER: 09/792,356
PRIOR PILING DATE: 2000-02-23
PRIOR PELICATION NUMBER: 08/477,639
PRIOR PILING DATE: 1955-06-07
PRIOR PILING DATE: 1955-06-07
PRIOR PILING DATE: 1955-06-07
PRIOR PILING DATE: 1955-06-07
PRIOR PILING DATE: 1995-02-01
PRIOR PILING DATE: 1995-02-01
PRIOR PILING DATE: 1995-04-07
PRIOR PILING DATE: 1995-04-07
PRIOR PILING DATE: 1995-04-20
PRIOR FILING DATE: 1990-04-20
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.0
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Fatent No. US2002009780A1
GENERAL INFORMATION:
APPLICANT: Dahiyat, Bassil
APPLICANT: Pilikov, Anton
TITLE OF INVENTION: USSIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
TITLE OF INVENTION: USSIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
TITLE OF INVENTION: USSIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
TITLE OF INVENTION: USSIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
TITLE OF INVENTION: USSIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
TITLE OF INVENTION: USSIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
TITLE OF INVENTION: USSIGN AND DISCOVERY OF TNF-ALPHA RELATED
CURRENT FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTION VET. 2.1
SEQ ID NO 13
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
Himmler, Adolph
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179 ECTKLC 184
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SOFTWARE: PATCHIN Ver. 2.1
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-798-789-13
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18.2%; Score 205.5; DB 9; Length 162;
Best Local Similarity 30.4%; Pred. No. 8.5e-09;
Matches 49; Conservative 20; Mismatches 71; Indels 21;
                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                      DB 9; Length 162;
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18.2%; Score 205.5; DB 9; Length 1
Best Local Similarity 30.0%; Pred. No. 8.5e-09;
Matches 48; Conservative 19; Mismatches 74; Indels
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Publication No. US20030130827A1
GENERAL INFORMATION:
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Patent No. US20020009780A1
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APPLICANT: Dahiyat, Bassil I.
APPLICANT: Desjarlais, John R.
APPLICANT: Hayes, Robert J.
APPLICANT: Vielmetter, Jost
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ORGANISM: Artificial Sequence
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APPLICANT: Hamptemann, Kudolph,
APPLICANT: Himmler, Adolph
APPLICANT: Himmler, Adolph
APPLICANT: Himmler, Adolph
APPLICANT: Stratewa Christian
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
TITLE OF INVENTION: Them
FILE REFERENCE: 98-385-J
CURRENT PELLORION NUMBER: 09/792,356
PRIOR PELLORION NUMBER: 09/792,356
PRIOR APPLICATION NUMBER: 08/477,639
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-02-01
PRIOR PILING DATE: 1995-02-01
PRIOR FILING DATE: 1995-02-01
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1992-01-02
PRIOR FILING DATE: 1990-04-20
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 16
LENGTH: 173
WANDER: DEA
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                                                                                                                                                                                                                                                                                    100 SQVALENCSAVADTRCGCKPGWFVECQ---VSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 QDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVEC---QVSQCV 131
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                                                                                                                                                                             40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
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                                                                18.2%; Score 205.5; DB 14; Length 162; 30.4%; Pred. No. 8.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 18.1%; Score 205; DB 9; Length 173; 1 Similarity 29.0%; Pred. No. 9.9e-09; 54; Conservative 23; Mismatches 85; Indels 2
                                                                                                                        71; Indels
                                                                                                                                                                                                                                                                                                                                                                                           157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                          20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/09899429A Patent No. US20020169118A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                        49; Conservative
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                                                                                            Best Local Similarity
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                US-10-218-102-430
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                                                                     Query Match
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APPLICANT: Dahiyat, Bassil I.

APPLICANT: Dahiyat, Bassil I.

APPLICANT: Dahiyat, Bassil I.

APPLICANT: Designatis, John R.

APPLICANT: Designatis, John R.

APPLICANT: Vielmetter, Jost
ITLE OF INVENTION: Protein Design Automation for Protein Libraries
FILE REFERENCE: A-6729-11/FF/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/218,102
FILE REFERENCE: A-6729-11/FF/RMS/RMK
CURRENT APPLICATION NUMBER: US 09/927,790
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 432
SOFTWARE: Patentin version 3.1
FENERTH PATOR FULL NUMBER: US 60/352,103
FENERTH PATOR FILING DATE: 2002-01-25
SOFTWARE: Patentin version 3.1
FILE OF INVENTION: Protein Design Automation for Protein Libraries
FILE REFRENCE: A-6729-11/RFY/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/218,102
CURRENT FILING DATE: 2002-08-12
FRIOR PRELICATION NUMBER: US 09/927,790
FRIOR FILING DATE: 2001-08-10
FRIOR PELING DATE: 2001-08-10
FRIOR APPLICATION NUMBER: US 60/311,545
FRIOR APPLICATION NUMBER: US 60/324,899
FRIOR FILING DATE: 2001-09-10
FRIOR PELING DATE: 2001-09-25
FRIOR APPLICATION NUMBER: US 60/351,937
FRIOR FILING DATE: 2002-01-25
FRIOR FILING DATE: 2002-01-25
FRIOR FILING DATE: 2002-01-25
FRIOR SEQ ID NOS: 432
SOFTWARE: Patentin Version 3.1
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18.2%; Score 205.5; DB 14; Length 162;
Best Local Similarity 30.0%; Pred. No. 8.5e-09;
Matches 48; Conservative 19; Mismatches 74; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 RDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 430, Application US/10218102
Publication No. US20030130827A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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OTHER INFORMATION: Description of Artificial Sequence: recombinant; OTHER INFORMATION: TNF-BP sequence
US-09-899-429A-10
                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
US-09-899-429A-10
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75 QDTFLAWENHHNSECARCOACDEOASQVALENCSAVADTRCGCKPGWFVEC---QVSQCV 131 15 LLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCP 74 24; Gaps Query Match 18.1%; Score 205; DB 9; Length 183; Best Local Similarity 29.0%; Pred. No. 1e-08; Matches 54; Conservative 23; Mismatches 85; Indels 셤 ò ò

S8 SGSFTASENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC- 115

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Search completed: June 27, 2005, 14:15:50 Job time : 165 secs

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61 CTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKFG 120
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PATENT NO. 6462176

GENERAL INFORMATION:

APPLICANT ABAKEMAZI, Avi J.

TITLE OF INVENTION:

ACRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

COUNTRY:

SOUTH SAN FRANCISCO

STREET: 1 DNA WAY

CITY: SOUTH SAN FRANCISCO

STREET: 1 DNA WAY

CITY: SOUTH SAN FRANCISCO

STREET: 1 DNA WAY

COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winheatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/928,069

FILING DATE: 11-Sep-1997

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: 60/026943

FILING DATE: 11-Sep-1997

CLASSIFICATION NUMBER: 35,600

REFERENCE/DOCKET NUMBER: 35,600

REFERENCE/DOCKET NUMBER: PLOSZRI

TELECOMMUTCATION INFORMATION:

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TELECOMMUTCATION INFORMATION:

TELECOMMUTCATION INFORMATION:

TELECOMMUTCATION INFORMATION:

TELEFRAX: 650/952-9881

INFORMATION POR SEQ ID NO: 1:

SEGUINGE CHARACTERISTICS:

LENGTH: 181 amino acids

TTYPE: Amino Acid
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100.0%; Pred. No. 1.7e-89;
iive 0; Mismatches 0;
                                  US-09-411-722-1

US-09-855-266A-1

US-08-477-347-14

US-08-477-347-14

US-08-477-347-14

US-08-476-862-5

US-08-828-683A-15

US-09-800-909-5

US-09-800-909-14

US-09-180-100-9

US-09-180-100-15

US-08-050-3198-4
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Sequence 1, Appli
Sequence 4, Appli
                                                                                                                                                                                                                                                                   June 27, 2005, 13:53:44; Search time 42 Seconds (without alignments) 346.585 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEQRPRGCAAVAAALLLVLL......CVSCPTSTLGSCPERCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
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Compugen Ltd.
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US-08-828-633A-1

US-08-477-347-12

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US-09-800-908-12

US-09-800-908-12

US-09-800-908-12

US-09-800-908-12

US-09-800-908-12

US-09-800-908-12

US-09-800-908-12

US-09-126-110

US-09-146-50-129

US-09-146-950-2

US-09-146-950-2

US-09-146-950-2

US-09-146-950-2

US-09-146-950-4

US-09-149-950-4

US-09-149-950-4

US-09-149-950-4

US-09-149-950-4

US-08-050-1198-5
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                                  GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                           protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-081-280-6_COPY_1_195
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Match Length DB
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Maximum DB seq length: 195
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Perfect score:
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Result No.

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TITLE OF INVENTION:
                        181 T 181
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                                                                                                                   US-08-219-237B-4
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61 CTEPCGNSTCLVCPQDTFLAWENHINSECARCQACDEQASQVALENCSAVADTRCGCKPG 120
                                                                                            121 WFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCP 180
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                                                                                                                                                                                                                                                                            ## Sequence 1, Application US/08828683A

## Sequence 1, Application US/08828683A

## GENERAL INCRMATION:
## APPLICANT: Ashkenazi, Avi J.

## TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
## NUMBER OF SEQUENCES: 28

** CORRESPONDENCE ADDRESS:

## ADDRESSES: Genentech, Inc.

** STREET: 1 DNA Way

## CITY: South San Francisco

## ATALE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 3.5-69-196
ATTORNEY/AGENT INFORMATION:
NAME: MARSCHANG, DIANE L.
REGISTRATION NUMBER: 35,60
REGISTRATION NUMBER: 35,60
REGISTRATION NUMBER: 35,60
REGISTRATION NUMBER: 91007PI
TELECOMPUNICATION: NUMBER: PI007PI
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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TYPE: Amino Acid
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INFORMATION FOR SEQ ID NO: 1:
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Matches 181; Conservative
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100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
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APPLICANT: NAGATA, Shigekazu
APPLICANT: TOW, Naoto
APPLICANT: TOWERARA, Shin
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE;
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
STREET: P.O. BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.7%; Score 200.5; DB 3; Length : 29.8%; Pred. No. 3.5e-11; tive 20; Mismatches 72; Indels
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,862
FLING DATE: 07-JUN-1995
CLASSIFICATION 1935
PRIOR APPLICATION NUMBER: IL 107267
FILING DATE: 12-OCT-1993
PRIOR APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION NUMBER: IL 91229
FILING DATE: 06-APR-1990
PRIOR APPLICATION NUMBER: IL 9129
FILING DATE: 06-ANG-1989
PRIOR APPLICATION NUMBER: IL 90339
FILING DATE: 10-ANA-1989
ATPONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPERENCE/DOCKET NUMBER: WALLACH=12A TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
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Patent No. 6270998
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amino acid
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                                                                                                            COMPUTER READABLE FORM:
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Best Local Similarity
Matches 48; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 153;
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                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,347
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17.7%; Score 200.5; DB 3;
Best Local Similarity 29.8%; Pred. No. 3.5e-11;
Matches 48; Conservative 20; Mismatches 72;
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FILING DATE:
FILING APPLICATION DATA:
APPLICATION UNBER: IL 106271
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSER: 34,033
REFERENCE/DOCKET NUMBER: 34,033
FILECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMATION INFORMAT
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                                                                                                                                                                                                                                ZIP: 20004
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 SEVENTH SELEEL, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08476862
Patent No. 626239
GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: BELETSKY, IGOR
APPLICANT: METT, IGOR
APPLICANT: METT, IGOR
APPLICANT: EBLESKY, IGOR
APPLICANT: ENGELMANN, Hartmut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: BROWDY AND NEIMARK
419 Seventh Street, N.W.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/115,685
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TELEX: 248633
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: TN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AN
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                                                                                                                                     Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-477-347-12
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US-08-476-862-3
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21; Gaps

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CORRESPONDENCE ADDRESS:
ADDRESSER: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                             WALLACH=12A
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APPLICATION NUMBER: 08/477,347
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GENERAL INFORMATION:
HEAD APPLICANT:
HEAD ACK
BELETSKY, IGOR
METT, IGOR
TITLE OF INVENTON: TNP LICANDS
NOMBER OF SEQUENCES: 17
                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APP-1990
PRIOR APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
PRIOR APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
PRIOR APPLICATION NUMBER: IL 90339
APPLICATION NUMBER: IL 90339
ATTORNEY/AGENT INFORWATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
REFERENCE/DOCKET NUMBER: MALLAC
APPLICATION NUMBER: 08/476,862 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 153 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 29.89
Marches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: peptide US-09-800-909-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 153;
  COUNTRY: USAN
ZIP: 22040-074
ZIP: 22040-074
COMPUTER ISADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,560C
FILING DATE: 06-UN-1995
CIASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WINREHY UR., GERLAD M.
REGISTRATION NUMBER: 20,4393P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEPAX: 703-205-8000
TELEPAX: 703-205-8000
TELEPAX: 703-205-8000
TELEPAX: 703-205-8050
TELEPAX: 733 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.7%; Score 200.5; DB 3; Best Local Similarity 29.8%; Pred. No. 3.5e-11; Matches 48; Conservative 20; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, Igor
APPLICANT: METT, Igor
APPLICANT: ENGELWANN, Hartmut
TITLE OF INVENTION: TNF INHIBITORS
UNMERS OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/800,909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 419 Seventh Street, N.W. CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09800909
Patent No. 6555111
GENERAL INFORMATION:
APPLICANT: WALLACH, David
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 153 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
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                                                                                                                                    40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                                                                                              9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                         Gaps
                                                                         21;
      DB 4; Length 153;
17.7%; Score 200.5; DB 4; Length 1
29.8%; Pred. No. 3.5e-11;
tive 20; Mismatches 72; Indels
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FILING DATE: 08-Mar-2001
CLASSIFICATION: <UNKNOWN>
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100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
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                                                                                                                                                                                                                                                                                                                                                                                     9 HPQNNSICCTKCHKGTYLXNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                                                                                                                                                                                    40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                           Query Match 17.7%; Score 200.5; DB 4; Length Best Local Similarity 29.8%; Pred. No. 3.5e-11; Matches 48; Conservative 20; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 EKONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 153
                                                                                                              TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-08-828-683A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 53, Application US/09523323
Patent No. 6635743
GENERAL INFORMATION:
     INFORMATION FOR SEQ 1D NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 154 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-523-323-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHINSECARCQACDEQA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 153;
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TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 EKONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 153
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FILING DATE: <Unknown>
APPLICATION NUMBER: IL 106271
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSENT GONGENT NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 34,033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 17.7%; Score 200.5; DB 4
Best Local Similarity 29.8%; Pred. No. 3.5e-11;
Matches 48; Conservative 20; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-800-908-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
FILING BATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08828683A Patent No. 6469144 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                            LENGTH: 153 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                 TELEX: 248633
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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APPLICANT: Willich, Stephen M.
APPLICANT: Ullrich, Stephen M.
APPLICANT: Ullrich, Stephen
APPLICANT: Diai, Yifan
APPLICANT: Diai, Yifan
APPLICANT: Diai, Yifan
TITER OF INVENTION: Apoptoeis Inducing Molecule II and Methods of Use
FILE REFERENCE: 1488.0656000C
CURRENT APPLICATION NUMBER: US/09/523,323
CURRENT APPLICATION NUMBER: 00/148,326
EARLIER APPLICATION NUMBER: 60/148,326
EARLIER FILING DATE: 1999-08-11
EARLIER FILING DATE: 1999-08-11
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-03-20
EARLIER FILING DATE: 1999-03-3-11
EARLIER FILING DATE: 1999-03-20
EARLIER FILING DATE: 1999-03-3-11
EARLIER FILING DATE: 1999-03-20
EARLIER FILING DATE: 1999-03-20
EARLIER FILING DATE: 1999-03-20
EARLIER FILING DATE: 1999-03-20
EARLIER FILING DATE: 1999-03-3
EARLIER FILING DATE: 1996-03-2
EARLIER FILING DATE: 1996-03-2
EARLIER FILING DATE: 1996-03-3
EARLI
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100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                                70 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
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  11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCDECESQSFTASENHLR-HCLSCSKCRKEM 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.6%; Score 198.5; DB 2; Length 154; 30.4%; Pred. No. 5.4e-11; tive 23; Mismatches 68; Indels 21
                                                                                                                                            157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                       157 RRDIDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: 8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CNORTWARE: Patentin Release #1.0, Version #1.30 CNORTWARE: Patentin NUMBER: US/08/23,087A FILING DATE: 08-SEP-1994 CLASSIFICATION: 435 CLASSIFICATION: 435 NAVE: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..154
OTHER INFORMATION: /note= "TNFR1, see Fig. 5"
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stein, Harald
APPLICANT: D rkop, Horst
APPLICANT: D at 2, Ute
TITLE OF INVENTION: Lymphoid CD30-Antigen
CORRESPONDENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22042
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Painner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 756-103P
TELECOMONINICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                Sequence 10, Application US/08232087A Patent No. S866372 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 amino acids
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Best Local Similarity 30.44
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STATE: Virginia
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                               JS-08-232-087A-10
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                          7;
                                                                                                                                                                                                       68 GOVEISSCIVDRDIVCGCRKNOYRHYWSENIFOC----FNCSLCLN-GIVH----LSCQ 117
                                                                                                                                                                100 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 156
                                                                      40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                   9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
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                          21; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09326394

Patent No. 6306820

GENERAL INFORMATION:
APPLICANT: Bendele, Alison M.
APPLICANT: Sennello, Regina M.
APPLICANT: Genarid, Carl K.
TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING
TITLE OF INVENTION: PROTEIN FOR TREATING TNF-MEDIATED DISEASES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 17.7%; Score 200.5; DB 3; Length 161; Best Local Similarity 29.8%; Pred. No. 3.7e-11; Matches 48; Conservative 20; Mismatches 72; Indels 21
                          Indels
                                                                                                                                                                                                                                                          157 RRDIDCGICLPGFYEHGDGCVSCPISTLGSCPE--RCAAVC 195
                                                                                                                                                                                                                                                                                         SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
1 Similarity 29.8%; Pred. No. 3.5e-11;
48; Conservative 20; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,587
FILING DATE: 06-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,355
FILING DATE: 23-0AN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,315
FILING DATE: 07-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/052,023
FILING DATE: 09-UUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Zindzick, Thomas K.
REGISTRATION NUMBER: 32,185
BEDDONNEY/ACKEN NUMBER: 32,185
BEDDONNEY/ACKEN NUMBER: 32,185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/326,394
FILING DATE: 08-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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ZIP: 91320-1789
Best Local Similarity
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US-09-326-394-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-326-394-2
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SEQ ID NO 2
LENGTH: 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: TAYLOR, J. Michael
APPLICANT: Kehrli, Jr., Marcus
APPLICANT: Kehrli, Jr., Marcus
APPLICANT: Ede, Eun-Kyung
APPLICANT: Wangi, Simon
TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: 08411-01801,
CURRENT APPLICATION NUMBER: US/09/513,007
CURRENT FILING DATE: 2000-02-25
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastESEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.3%; Score 196; DB 3; Length 139; 31.5%; Pred. No. 8.2e-11; Live 17; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 191; DB 4; Length 181; ; Pred. No. 3.1e-10; 17; Mismatches 76; Indels
119 KQNTVC-TCHAGFPLRENECVSC----GNCKKSLECTKLC 153
                                                                                                                                                                                                                                                                                 | SECULT | SECULT | SECULT | SECULT | SECULT | SECULT | SECUL | SECULT | SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 RRDTDCGTCLPGFYEHGDGCVSC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 129, Application US/08706945D Patent No. 6369027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09513007
Patent No. 6406907
GENERAL INFORMATION:
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Best Local Similarity 31.5%
Matches 45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-706-945D-129
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Best Local Similarity
                                                                                                                                                      RESULT 13
US-08-706-945D-129
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40 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 99

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Sequence 2, Application US/09146950A
Patent No. 6287808
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FARLSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 PGTYIA---HLNGLSKCLQCQMCDPAMGLRASRNCSRTENAVCGCSPGHF-----CIV 129
                                                                                                     100 SQVALENCSAVADTRCGCKPGWFVBCQVSQCVSSSPFYCQPCLDC--GALHRHTRLLC-S 156
                                                                                                                                                  81 FQVEISPCVVDRDTVCGCRKN----QYRBYMGETGFRCLNCSLCPNGTVN----IPCQE 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 QDTFLAWENHHN - - SECARCOACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVS 132
22 HPQNSTICCTKCHKGTYLYNDCPGPGRDTDCRVCAPGTYTALENHLA-RCLSCSRCRDEM 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 LYLTFLGAPCY----APALPSCKEDEYPVGSECCPKCSPGYRVKEACGELTG-TVCEPCP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 SSPFYCQPCLDCGALHRHTRLL---CSRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 LLLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
16.5%; Score 186; DB 3; Length 193;
Best Local Similarity 29.2%; Pred. No. 9.7e-10;
Matches 52; Conservative 16; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                      157 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPERC 191
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Job time : 49 secs
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ORGANISM: Homo sapiens
US-09-146-950-2
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ferredoxin-type pr
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                                              June 27, 2005, 14:04:00 ; Search time 38 Seconds (without alignments) 440.571 Million cell updates/sec
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                                                                                                1 QGGTRSPRCDCAGDFHKKIG......CPTSTLGSCPERCAAVCGWR 174
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Compugen Ltd.
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GenCore version (c) 1993 - 2005
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                               - protein search, using sw model
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1: pir1:*
2: pir2:*
3: pir3:*
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seq length: 174
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Match 1
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Perfect score:
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metallothionein 3 metallothionein-II keratin hich-sulfu:	metallothionein II probable oxidoredu probable oxidoredu hypothetical prote NapF Ferredoxin co	metallothionein-li metallothionein II electron transport finger protein (cl	growth inhibitory metallothionein 3, high-cysteine chor probable oxidoredu	тs	sulfur matrix protein	:t-1999 #text_change 09-Jul-2004	December 1991 of a Human high-aulphur keratin cDNA.		1755; NID:g32471; PIDN:CAA45283.1; PID:g32472 5.	or a class of cysteine-rich proteins of the PMID:1703541	NDN:CAA39005.1; PID:934079						F;118-126/Region: Ser-rich nonapeptide repeat F;127-136/Region: Cy8-rich decapeptide repeat F;137-145/Region: Ser-rich nonapeptide repeat F;146-155/Region: Cy8-rich decapeptide repeat F:156-165/Region: Cy8-rich decapeptide repeat	. DB 1; Length 169; 0.58; thes 71; Indels 56; Gaps 12;	CCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACD 72	EQASQVALENCSAVADTRCG-CKPGWFVECQVSQCVSSSPFYCOPCLDCGALH 124
S44392 T07090 KRGT3.T	T15610 T15610 T15610	A55011 T05719 H75154 S06557	167866 A46034 A21761 B83410	ALIGNMENTS	an 1tra high-s	ision 22-0c	y, December e of a Huma		4; EMBL:X63 Rogers, G.E	of genes f 91115951; P	D:934078; P	MIM:148021	keratin	de repeat ide repeat	ide repeat	ide repeat tide repeat ptide repea	ptide repea ptide repea ptide repea ptide repea	Score 103; D Pred. No. 0.5 6; Mismatches	PCTEPCGNSTCLVCF : : -CGSSCGGCDSSCGSC-	G-CKPGWFV
			0000		human n; ult	rev	orar Jenc		1456	ion JID:	AAC,	0	nr	at epti ept	ept ept	oept apep sape	appe Sape	46 46	repc 	OTRC
68 85	131 131 135 166	69 166 168	68 124 153		in 1 - keratir	squence squence 36686	e, D. Data Lil Ide sequ 3946		IPROT:Q	express	1-169 <p< td=""><td>3:12525</td><td>igh-sul</td><td>am repea n nonape ch decar</td><td>th decay</td><td>ch nonay ich deca rich dec</td><td>rich der</td><td>9.9% larity 25.3% Conservative</td><td>HYLKAPC C</td><td>ENCSAVAI</td></p<>	3:12525	igh-sul	am repea n nonape ch decar	th decay	ch nonay ich deca rich dec	rich der	9.9% larity 25.3% Conservative	HYLKAPC C	ENCSAVAI
	4.6.6.6.6				ır keral se: UHS	84D1en 1999 #80 3946; B.	Doeneck EMBL 1 Wucleot:	1946 : mRNA 59 < DRA:	J.; Power	ire and	DNA 9,'Y',4:	L ses: GD	11q13-	r, tand Ser-rich Glv-rich	Gly-ric	Ser-ri : Cys-r: 1: Cys-:	h: Ser-	Similarity 5; Conser	CCRGCPAGI	DASQVALI
77.5 77	76.5 76 76 76 75.5	7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	74.5 74.5 74.5		RESULT 1 818946 ultra high-sulfur keratin 1 N/Alternate names: UMS kera	122-Oct-1	tt, B.; I d to the ption: I	lon: Signal Signature (19 1)	reference mon, P.	Structi	le type les: 1-3 referen	.cs: GDB:KRN: referen	sition:	de: hai legion: { Region:	Region: Region:	Region: /Region 7/Region	6/Region 6/Region 5/Region 5/Region 5/Region	Match Local Sin	о—о г г	73 E
30	1 W W W W W W W W W W W W W W W W W W W	3 6 6 4 4 5 8 6 0 1 5	4 4 4 4 0 6 4 0		RESULT 1 S18946 ultra hi N;Altern	; Specie ; Date:	A;Draber submitte A;Descri	A;Access A;Molecu A:Residu	Cross-	Title:	Molecu N, Melecu N, Residu N, Cross-	;;Geneti ,;Gene: ,;Cross-	, Map pc	7, Keywor 7,7-15/F	7;69-78/	,89-97/ ,98-107 ,108-11	7,118-12 7,127-13 7,137-14 7,146-15	Query M Best Lo Matches	s d	ò

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Cipacession: B21761
R; Iatrou, K.; Tsitilou, S.G.; Kafatos, F.C.
Proc. Natl. Acad. Sci. US.A. 81, 4452-4456, 1984
A; Ttile: DNA sequence transfer between two high-cysteine chorion gene families in the sill A; Reference number: A21761; MUID:84272653; PMID:6589605
A; Accession: B21761
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-143 <IAT>
C; Superfamily: chorion class A protein pc292
                                                                                                                                                                                                                         Cispecies: Tetrahymena pigmentosa
Cispecies: Soulise: Soul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 ENHINSECARCOACDEDASOVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 ENRYKGDVC---VCGEVPFLGTADVCGNMCSSGCGCID-----YGCGNGCVGITRSC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 CTGTGEGCKCTGCKCCQPAKSGCCCGDKAKACCTDP--NSGC-CCSSKTNKCCDSTNKTE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 CDCAGDFHKKIGLFCCR----GCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 CGC------CCRGCGCG-----CGGCGCCCENFRVCSNSAAPIGLSICS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              high cysteine chorion B 12 protein precursor - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cysteine-rich hair keratin associated protein - rabbit
C;Species: Oryccolagus cuniculus (domestic rabbit)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: 146489; S49201
GQPCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSSKCRRCRLCDE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GCGGC-----GCGCGGC-----GCCGCSCGRSC 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 94.5; DB 2; Length 104; Pred. No. 1.8; 8; Mismatches 29; Indels
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                                                                                                                                                                                                metallothionein-2 - Tetrahymena pigmentosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 9.1%;
1 Similarity 34.3%;
23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Genetic code: SGC5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S:
Matches 23,
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                                                                                                                                                                                                                                                                                                                               trophozoite surface antigen - Giardia lamblia (strain Adelaide-1) (fragment)
C;Species: Giardia lamblia
C;Species: Giardia lamblia
C;Date: 14-Uul-1994 #sequence_revision 14-Uul-1994 #text_change 09-Uul-2004
C;Accession: PC1294
R;EY, P.L.; Mayrhofer, G.
Gene 129, 257-262, 1993
A;Title: Two genes encoding homologous 70-kDa surface proteins are present within indivi
A;Reference number: PC1294; MUID:93314970; PMID:8325510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fas-Delta-(4,7) protein - human
Cispecies: Homo sapiens (man)
Cipacies: Homo sapiens (man)
Cipacession: S58662; S57566
R;Liu, C.; Cheng, J.; Mountz, J.D.
R;Liu, C.; Cheng, J.; Mountz, J.D.
A;Title: Differential expression of human Fas mRNA species upon peripheral blood mononuc
A;Reference number: S58662; MUID:96013198; PMID:7575433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 CYETVKYPĠKTV-----CISAPNGGTĊQKAADGYKLDSGTLTVĊSEGCKECTSSTDĊTT 110
PVCCCVPACSCSSCGKRGCGSCGGSKGGCGSCGCSQCSCCKPCCCSSGCGSSCCQCSC-- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26
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                                                                             125 RHTRLLCSRRDTDCGTCLPGFYEHGDG---CVS-----CPTSTLGS--CPERCAAVC 171
                                                                                                                      -----CKPYCSQCSCCKPCCSSSGRGSSCCKPCCSSSGCGSSCCKPC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P21849; GB:M97488; NID:g159129; PID:g159130 C;Genetics:
C;Genetics:
A;Gene: tsa
C;Keywords: surface antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 9.3%; Score 96.5; DB 2; Length 141; Local Similarity 27.2%; Pred. No. 1.5; nes 41; Conservative 10; Mismatches 65; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1-149 <LIU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.2%; Score 96; DB 2; Length 149; Best Local Similarity 33.3%; Pred. No. 1.7; Matches 18; Conservative 7; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 «SCH»
A;Cross-references: EMBL:X89101; NID:g887457; PID:g887458
C;Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 CLPGFYEHGDGCVSCPTS--TLGSCPERCAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 CLDGYVKSASACTKCDSSCETCNGAATTCKA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: UNIPROT:P25445
R;Schatzlein, C.E.
submitted to the EMBL Data Library, June 1995
A;Reference number: S57565
A;Accession: S57566
A;Status; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-141 < EYP>
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NiAlternate names: M2.6 protein
C;Species: Capra aegagrus hircus (domestic goat)
C;Species: Capra aegagrus hircus (domestic goat)
C;Accession: B92978; A02840
R;Joubert, P.J.
J. S. Afr. Chem. Inst. 28, 250-263, 1975
A;Title: Studies on the high-sulphur proteins of reduced mohair. The isolation and the an
C;Accession: S60314
R;Fratini, A.; Powell, B.C.; Hynd, P.I.; Keough, R.A.; Rogers, G.E.
J. Invest. Dermatol. 102, 178-185, 1994
A;Title: Dietary cysteine regulates the levels of mRNAs encoding a family of cysteine-ric A;Reference number: S60314; MUID:94149288; PMID:7508963
A;Retension: S60314
A;Status: preliminary
                                                                                                                                                                                                                          A;Molecule type: mRNA
*Residues 1-151 - FRBA-
A;Cross-references: UNIRROT:028576; EMBL:X73462; NID:9512030; PIDN:CAA51841.1; PID:951203
C;Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 -ISSCYRPSCCRSSCGSSCY---RPTSCISSCCRPQCCQPVCCQPSGA-----RISSCCR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 CICSECGKSFTDHAGLRIHQKYHTGVKPFSCSECGKCFTRRS----GLTAHLRIHTGEK 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 ALENCSAVADTRCGCKPGWFVECQVSQCVSS--SPFYCQP--CLDCGALHRHTRLLCSRR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 CGNSTCLVCPOD--TFLAMENHHNS----ECARCOACDEQASOVALENCSAVADTRCGCK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             finger protein (clone XlcGF42-1) - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GEKPYSCSDCGKCFTRRWNLSEHRKSHTGQKRFCCSVCGKGFSYHSQMKSHYRTHTGEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCR-GCPAGHYLKAPCTEP-CGNSTCL--VCPQDTFLAWENHHNSECARCQACDEQASQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 CCRPSCCQTTCCRTTCYRPSCGVSSCCRPICCQPT-----CPRPTCC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 PGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGD 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          keratin high-sulfur matrix protein IIIA3, minor component - goat
                                                                                                                                                                                                                                                                                                                                                                     ch 8.3%; Score 86; DB 2; Length 151; 1 Similarity 24.8%; Pred. No. 9.4; 38; Conservative 14; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 8.1%; Score 84.5; DB 2; Length 1 Similarity 23.3%; Pred. No. 13; 41; Conservative 13; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 PSCCGSSC----YRPSCCLRPVCNRVSCHTTC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 DIDCGTCLPGFYEHGDGCVSCPTSTLGSCPERC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-168 <NIE>
A;Cross-references: UNIPROT:P18720
C;Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type:
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Best Local S
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Matches 3
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                                                                                                                                                                                                                             A;Residues: 1-126 <POW>
A;Cross-references: UNIPROT:Q28707; EMBL:X80035; NID:g510540; PIDN:CAA56339.1; PID:g5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Estredaxin-type protein NapF [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Versinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Juj-2004
C;Accession: AG0369
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; II, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: Ab0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q8ZCF1; GB:AL590842; PIDN:CAC92282.1; PID:g15980993; GSPDB:q
         R,Powell, B.C.; Arthur, J.; Nesci, A.
Differentiation 58, 227-232, 1995
A;Title: Characterization of a gene encoding a cysteine-rich keratin associated protein A;Reference number: 146489; MUID:95228955; PMID:7536172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 QACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 NCSAVADTRCGCKPGWFVECQVS-QCVSSSPFYCQPCLD-CGALHRHTRLLCSR---- 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68
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S60314
S60314
C;63pecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;8pecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;8pecies: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 CGQDFCQEES----CRPSC-----CRPQCCQPSCCRPTCCI-----SSCCRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 CAGDFHKKIGLFCCR-GCPAGHYLKAPCTEP-CGNSTCLVCPQDTFLAWENHHNSECARC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: napF
C;Superfamily: ferredoxin protein NapF; ferredoxin 2[4Fe-4S] homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 QCCQ-----SVCCQPTC-CRP----SCYISSC--CRPTCCRP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 LLCSR----RDTDCGT-----CLPGFYEHGDGCVS--C-PTSTLGSC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 -rccrprccrprscorrccrroccrpsc-----cvsrccrpccssgsc 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
8.5%; Score 88; DB 1; Length 167;
Best Local Similarity 23.2%; Pred. No. 7.1;
Matches 36; Conservative 18; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 126;
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                                                                                                                    A;Accession: 146489
A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                           8.7%; Score 90; DB 2
25.4%; Pred. No. 4.3;
tive 9; Mismatches
                                                                                                                                                                                                                                                                                                                     A,Gene: KAP4L
C,Superfamily: ultra-high-sulfur keratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 43; Conserv
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A; Residues: 1-167 < KUR>
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A; Status: preliminary
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A,Title: Mouse cellular nucleic acid binding proteins: a highly conserved family identifi A,Reference number: A55499; MUID:95203870; PMID:7896269
A,Accession: 148299
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-171 - ARES-
A,Cross-references: UNIPROT:P53996; EMBL:Z11871; NID:950474; PIDN:CAA77897.1; PID:950475
C,Superfamily: cellular nucleic acid-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Accession: A55499
R;Warden, C.H.; Krisans, S.K.; Purcell-Huynh, D.; Leete, L.M.; Daluiski, A.; Diep, A.; Te Genomics 24, 14-19, 1994
A;Title: Mouse cellular nucleic acid binding proteins: a highly conserved family identif; A;Reference number: A55499; MUID:95203870; PMID:7896269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148297
cellular nucleic acid binding protein clone 6 - mouse
c;Species: Mus musculus (house mouse)
C;Date: 02-7ul-1996 #sequence revision 02-7ul-1996 #text_change 09-Jul-2004
C;Accession: I48297; S19861; S19959
R;Warden, C.H.; Krisans, S.K.; Purcell-Huynh, D.; Leete, L.M.; Daluiski, A.; Diep, A.; Ts
Genomics 24, 14-19, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 NHHINSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 HHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLD 119
                                                                                                                                                                                                                                                                                                                                                                                                                   105 DHADE-QKCYSCGEFGH--IQXDCTKVKCYRCG-ETGHV----AINCSKTSEVNCYRCGE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 RCDCAGDFHKKIGL--FCCRGCPAGHYLKAPCTEP----CGNSTCLVCPQDTFLAWEN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                8 RCDCAGDFHKKIGL---FCCRGCPAGHYLKAPCTEP-----CGNSTCLVCPQDTFLAWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L12693; NID:g292347; PIDN:AAA89198.1; PID:g292348
                                                                                                                                                                                                                                                              Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 8.0%; Score 83; DB 2; Length 170; Local Similarity 27.0%; Pred. No. 17; hes 34; Conservative 13; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                         59; Indels
                                                                                                                                                                                                                                                              Query Match
8.0%; Score 83.5; DB 2;
Best Local Similarity 26.8%; Pred. No. 15;
Matches 34; Conservative 13; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:125342; OMIM:116955
A;Map position: 3q13.3-3q24
C;Superfamily: cellular nucleic acid-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    zinc finger protein 9 - human
N;Alternate names: nucleic acid binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | | |
157 ESGHLAR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DCGALHR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGALHR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCHLAR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-170 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: GDB: ZNF9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
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                                                                                                                                         A; Experimental source: Angora breed
C; Comment: Wool and hair consist of microfibrils embedded in a rigid matrix of other pro
C; Superfamily: keratin high-sulfur matrix protein IIIA
C; Keywords: duplication; hair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-152 <ROG>
A;Cross-references: UNIPROT:Q29620; GB:L33888; NID:g499874; PIDN:AAB01447.1; PID:g940358
C;Superfamily: keratin high-sulfur matrix protein IIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cellular nucleic acid binding protein clone 14 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 148298; S19960
R;Warden, C.H.; Krisans, S.K.; Purcell-Huynh, D.; Leete, L.M.; Daluiski, A.; Diep, A.; Genomics 24, 14-19, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 CPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 -QAVVCRPC--CWA-----TTC--CQP-----VSVQCPCCRPTSCQPAPC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 CSAVADTRCGCKFGWFVECQV-----SQCVSSSFFYCQP------CL---- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 SSPFYCOPCLDCGALHRHTRLLCSRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSC-PERC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 CQPTCLQTSGCKTGCGIGGSIGYGQVGSSGAVSSRTRWCRPDCRVEGTSLPPCCVVSCTS 104
                                                                                                                                                                                                                                                                                                                                                                                                  2 GGTRSPRC---DCAGDFHKKIGLFCCRGCPAGHYLKAP-----CT----EPCGNSTCLV 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 GGCLQPRCYRDPC-----CCRPVSCQTTVSRPVTFVSRCTRPICEPCRRPVC-- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 ------CRP---ITCCPTSC-- 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 CCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALEN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CCSTSFCGFPI-CPTAGTCGSSCC------RSTCSQTSCC--QPTSIQTSC 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C, Date: 21-Feb_1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 - DCGALHRHTRLLCSRRDTDCG--TCLPGFYEHGDGCVSCPTSTLGSCPERCA-AVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSCCQLYYAQASCC--RPSYCGQSCCRP----ACCCQPTCTEPVCEPTCSQPIC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C)Accession: 147108
R;Rogers, G.R.; Hickford, J.G.; Bickerstaffe, R.
Anim. Genet. 25, 407-415, 199 genes for B2 high sulfur proteins of wool.
A;Reference number: 147105; MUID:95209146; PMID:7695121
A;Accession: 147108
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                   91;
                                                                                                                                                                                                                                                                                        Length 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68; Indels
                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                     Score 83.5; DB
Pred. No. 13;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
8.0%; Score 83.5; DE
Best Local Similarity 22.0%; Pred. No. 14;
Matches 39; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           high-sulfur wool matrix protein B2C - sheep
                                                                                                                  Cross-references: UNIPROT: P02442
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.8%;
                                                                                                                                                                                                                                                                                                                                             42; Conservative
  A; Reference number: A92978
                          A; Accession: B92978
A; Molecule type: protein
A; Residues: 1-131 <JOU>
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Matches
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Title: Mouse cellular nucleic acid binding proteins: a highly conserved family identif
Reference number: A55499; MUID:95203870; PMID:7896269
Accession: 148297
                                                                                                                                                                                           R;Warden, C.H.
submitted to the EMBL Data Library, January 1992
A;Description: Cellular nucleic acid binding protein (CNBP) is an extremely conserved cy
A;Recenson: S19861
A;Accession: S19861
                                                                                                               A;Molecule type: mRNA
A;Residues: 1-170 <RES>
A;Cross-references: UNIPROT:P53996; EMBL:Z11870; NID:G50472; PIDN:CAA77896.1; PID:G50473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: UNIPROT:09XVB0; EMBL:281493; PIDN:CAB04040.1; GSPDB:GN00020; CESP:FG; Experimental source: clone F01D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.9%; Score 82.5; DB 2; Length 133;
Best Local Similarity 24.0%; Pred. No. 16;
Matches 36; Conservative 11; Mismatches 44; Indels 59; Gaps 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 DHADE-QKCYSCGEFGH--IQKDCTKVKCYRCG-ETGHV----AINCSKTSEVNCYRCGE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 HHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLD 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- AKOGYCTSCFLDCAEKIO 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 RCGESGHLAKDCDLQEDACYNCGRGGHIAKDCKEPKREREQC----CYNCGKPGHLARDC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 RCDCAGDFHKKIGL - FCCRGCPAGHYLKAPCTEP - - - - CGNSTCLVCPQDTFLAWEN 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 PLADC----HAYAGL--CSNPMYTSFLDKYCPKTCG-----LCPDSTTL------ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nypothetical protein F01D5.2 - Caenorhabditis elegans
Species: Caenorhabditis elegans
Spotses: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-170 <WA2>
A;Cross-references: EMBL:X63866; NID:g50470; PIDN:CAA45345.1; PID:g50471
C;Superfamily: cellular nucleic acid-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted to the EMBL Data Library, November 1996
A;Reference number: 219279
A;Accession: T20467
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-133 <WIL>
                                                                                     Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
8.0%; Score 83; DB 2
Best Local Similarity 27.0%; Pred. No. 17;
Matches 34; Conservative 13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: June 27, 2005, 14:19:24 Job time : 40 secs
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A;Map position: 2
A;Introns: 81/2
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32; Conservative
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150 AA;
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Receptor.
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Query Match
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Q8MJ20
ID Q8MJ
AC Q8MJ
DT 01-0
                                                                                                                             RESULT 1
Q9R230
8
                                                                                                                                                                                                                                                                                     Q9r230 rattus norv Q8r320 macaca mula Q7zzy gallus gall Q8sq5 felis silve Q9jke0 rattus norv Q8sq49 felis silve
                                                                                                                                                                                                                                                                                                                                                                                                                                               human cytom
human cytom
camelpox vi
human cytom
mus musculu
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bombyx mori
branchiosto
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human cytom
homo sapien
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cowpox viru
vaccinia vi
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drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xenopus lae
cowpox viru
                                                                                                                                                                                                                                                                                                                                     paramecium
                                            June 27, 2005, 14:05:01; Search time 173 Seconds (without alignments) 515.039 Million cell updates/sec
                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                         Description
                                                                                     1 QGGTRSPRCDCAGDFHKKIG......CPTSTLGSCPERCAAVCGWR
                                                                                                                                                                                                                                                                                                         088952
088951
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057093
      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                       1612378 segs, 512079187 residues
                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                       Q6ITV8
Q9DJL2
KRUA HUMAN
O72762
Q8UYL3
Q14564
Q8BDC3
Q8BDC4
Q6SC66
                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                protein search, using sw model
                                                                       US-10-081-280-6_COPY_25_198
1038
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08S052
08S051
09JKE0
08S049
09BIR2
09BIR3
                                                                                                                                                                                                                                                                                                                                                         Q8BDC5
Q911R0
Q6P2H9
Q8BDC6
Q8WT16
Q7TFH9
                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                09N2N0
                                                                                                                                                                                               UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
            Copyright
                                                                                                                                                 seq length: 0
seq length: 174
                                                                       Title:
Perfect score:
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111.5
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                                             Run on:
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homo sapien
homo sapien
oryza sativ
       mus musculu
                                                                       tetrahymena
                                                                                                           tetrahymena
                                                                                                                                           xenopus lae
tetrahymena
                                                                                                                                                                                                     rhodobacter
rhodobacter
                                                                                                                                                                                                                                                                                                             homo sapien
                                                                                                                                                                                                                                                                             drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                       Domor
                            09byq4
P80394
P80394
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O91388
O93022
O9738
O67119
O67119
O671898
O671898
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O67189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Careau R.R., Dharmarajan A.;

La Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF104034; AAD20221.1; -.

EMBL; AF104034; AAD20221.1; -.

RGO; GO:0016020; C:membrane; IEA.

GO; GO:00006915; P:apoptosis J. IEA.

GO; GO:00006915; P:apoptosis J. IEA.

RGO; GO:0007165; P:signal transduction; IEA.

R InterPro; IPR008063; Pas receptor.

R InterPro; IPR001369; TNFR_C6.

R Pfam; PF00020; TNFR_C6.

R Pfam; PF00020; TNFR_C6; Z.

R SMAT; SM00208; TNFR, Z.

R PROSITE; PS00626; TNFR_Z, Z.

R PROSITE; PS00626; TNFR_Z, Z.

R PROSITE; PS00620; TNFR_Z, Z.

R PROSITE; PS00650; TNFR_Z, Z.

R P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 VALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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16644 MW; 7DEC76EC40A6BA4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.9%; Score 165.5; DB 2
30.8%; Pred. No. 1.7e-06;
tive 13; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ź
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
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Q9D732
KR92 HUMAN
MT1 TETP1
MT1 TETP7
Q915J3
MT1 TETPY
083722
Q9RAD6
                                                                                                                                                                                                                                                                      Q6Y1L9
Q6L8G8
Q6L8G9
KR42 HUMAN
Q8RYZ5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2003 (TrEMBLrel. 24, Fas receptor (Fragment).
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59 NHHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 CSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDC--- 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------KHTECPPGF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 CRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQA-CDEQASQVALEN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 DCGALHRHTRLLCSRRDTDCGTCLPGFYEHG--DGCVSCPTSTLGSCPERCAAVCGW 173
                                                                                                                                                                                                                                                                                                                                                                                                    -----EHGILENCT--PISNT-KCKQGSSSKLLW 90
                                                                                                                                                                                                                                  Query Match 14.1%; Score 146.5; DB 2; Length 146; Best Local Similarity 28.3%; Pred. No. 6.6e-05; Matches 39; Conservative 13; Mismatches 49; Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
"Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fas (Fragment).
Belis silvostris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 13.0%; Score 135; DB 2; Length 147; Local Similarity 27.4%; Pred. No. 0.00062; nes 32; Conservative 15; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016020; C:membrane; IEA.
GO; GO:0004888; F:tranamembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0007165; P:signal transduction; IEA.
InterPro; IPR008063; Pas receptor.
InterPro; IPR008063; TNFR_C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 147 147 147 MW; OE192AC4DCE1001F CRC64;
                                                                                                                                                                     146 AA; 16487 MW; 1C9E64FE3A0FC2DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8SG52;
01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-UNR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00020; TNFR c6; 2.
PRINTS; PR01680; FASRECEPTOR.
SMRAT; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 1.
PROSITE; PS50050; TNFR NGFR 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J. Immunogenet. 31:159-166(2004).
EMBL; AB072009; BAB6798.1; -.
HSSP; 014763; 1D4V.
SMART; SM00208; TNFR; 3.
PROSITE; PS01186; EGF 2; UNKNOWN 1.
PROSITE; PS00505; TNFR_NGFR 1; 1.
PROSITE; PS50050; TNFR_NGFR-2; 2.
NON TER 146 146
SEQÜENCE 146 AA; 16487 MW; 1C9E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:: | | | |:: |: | 97 CTSTQDRVCECIEGWYLELEF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 GTCLPGFYEHGDGCVSCP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 GVAQPGTPESDTVČFCČP 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON TER
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINEL STACE TO THE PROPERTY OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 GOFCRNPCPPGERKARDCTVNEDEPDCVPCQEGKEYTDKGHFSSKCRRCRLCDEGHGLEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Petit F., Arnoult D., Lelievre J.-D., Lecossier D., Hance A.J.,
Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 15.6%; Score 161.5; DB 2; Length 130; Local Similarity 31.7%; Pred. No. 3.3e-06; nes 32; Conservative 12; Mismatches 50; Indels 7
                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                    Estaquier J.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AFS30075; AAM95635.1; -.
HSSP; 014763; 1DU3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016020; C:membrane; IEA.
GO; GO:0004888; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0007165; P:isignal transduction; IEA.
InterPro; IPR008063; Faa receptor.
InterPro; IPR008063; Faa receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 AA; 14814 MW; 91542C61323F3C27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 LENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 BINCTRIONTKCRCKPNFF-----CNSAVCEHCDPCTKC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Osteoprotegerin (Fragment).
      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Fas receptor CD9 (Fragment).
Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00020; TNFR_c6; 2.
PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 2.
PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
                                                                                                                                                                                                                                  NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor.
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Q8SQ49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 SHPSPRCRRCKICDEEHGLEVERNCTRTQNTKCRCKSNFF--CNVSQC-----DHCNPCM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Wistar; TISSUE=Smooth muscle; MEDINE-99330195; Pubmed=10403401; DOI=10.1016/S0014-5793(99)00683-3; Krzesz R., Wagner A.H., Cattaruzza M., Hecker M.; "Cytcokine-inducible CD40 gene expression in vascular smooth muscle cells is mediated by nuclear factor kappaB and signal transducer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
"Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
                                                                                                                                                                                                                                                                                      Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.9%; Score 133.5; DB 2; Length 124; 29.4%; Pred. No. 0.00072; ive 12; Mismatches 23; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 DCGALHRHTRLLCSRRDTDCGTCLPGFYEHG--DGCVSCPTS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0016020; C:membrane; IEA.
GO; GO:0004888; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0007165; P:immune response; IEA.
InterPro; IPR008063; Fas receptor.
InterPro; IPR008063; Fas receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 AA; 14319 MW; 15A7DFF058D79942 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                         124 AA
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PROSITE; PS00652; TNFR NGFR_1; UNKNOWN_1.
PROSITE; PS50050; TNFR_NGFR_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eur. J. Immunogenet. 31:159-166(2004).
EMBL; AB072010; BAB86799.1; -.
HSSP; 014763; 1D0G.
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SEQUENCE FROM N.A.
STRAIN=Wistar; TISSUE=Smooth muscle;
                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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FEBS Lett. 453:191-196(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001368; TNFR c6. Pfam; PF00020; TNFR c6; 2. PRINTS; PR01680; FASRECEPTOR.
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                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                   Fas delta6 (Fragment).
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SEQUENCE
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RESULT 5
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66 ARCQACD-EQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLD---CG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 QCVTCSDKQYLQGGECCDLCQPGNRLVSHCT-ALEKTQCQPCDSGEFSA---HWNREIRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Mizuno T., Baba K., Goto Y., Masuda K., Ohno K., Tsujimoto H.;
"Alternatively spliced transcripts of Fas mRNAs in feline lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fas delta 5 delta 6 (Fragment).
Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
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                                                                                                                                                                                  GO; GO:0016220; C:membrane; IEA.
GO; GO:0016220; C:membrane; IEA.
GO; GO:0006915; P:stansmembrane receptor activity; IEA.
GO; GO:0006915; P:stapptoclasis; IEA.
GO; GO:0006915; P:stamme response; IEA.
GO; GO:001165; P:stanal transduction; IEA.
InterPro; IPR0010865; Rabosomal_S2.
InterPro; IPR0011865; Ribosomal_S2.
InterPro; IPR0011865; Ribosomal_S2.
InterPro; IPR001208; INFR_G5.
PERM; PR011869; PASRECEPTOR.
SMART; SM00208; TNFR; 3.
Krzesz R., Hecker M.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                             SEQUENCE FROM N.A., STRAIN=Wiscle; STRAIN=Wistar; TISSUE=Smooth muscle; Gao D., Hecker M.; Submitted (MAR-201) to the EMBL/GenBank/DDBJ databases. EMBL; AF241311, AAF43717.2; -. HSSP; Q92956; 1JMA.
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EMBL; AB072012; BAB86801.1; -.

EMBL; AB072012; Chembrane; IEA.

GO; GO:0006915; P:transmembrane receptor activity; IEA.

GO; GO:0006915; P:apoptosis; IEA.

GO; GO:0006955; P:immune response; IEA.

GO; GO:0007165; P:sigmal transduction; IEA.

InterPro; IPR008063; Ras receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 PGFGVVQMATETTDTVCQPCPVGFFSNG 154
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PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 1.
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Best Local Similarity
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34; Conservative
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Matches 27; Conserva
                                                                                                                                                                                                                                             Local Similarity
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NCBI_TaxID=44088;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=CNPV086;
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Q6VZR1;
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Q8BDC5
ID Q8BDC
                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                     59 NHHNSECARCOACDEDASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 CQACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHT 127
                                                                                                                                                                                                10 SHPSPRCRRCKICDEEHGLEVEKNCTRIQNIKCRCKSNFF--CNVSOC----DHCNPCM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 CQP-----GLNRIIDNVNNKCNCLDGYYETTGVLACTQCSP----PCYDC----- 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 RCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECAR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 KCICSSNYYSQLSSLVCRAC----ISPCLECLDDA--LALPAD-----GTQCVT 47
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name-fur;
Paramecium aurelia.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
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                                                                                                                         7;
                                                                     Query Match 12.2%; Score 126.5; DB 2; Length 65; Best Local Similarity 36.7%; Pred. No. 0.0016; Matches 22; Conservative 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.0%; Score 125; DB 2; Length 110; 22.4%; Pred. No. 0.0034; ative 17; Mismatches 52; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=2998-axenic;
Wyroba E., Wiejak J., Surmacz L.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF351195; AAK27160.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER 1 1 1 NON TER 110 NON TER 110 NON TER 110 A4, 11810 MW, 449E0D07D8BB0A91 CRC64;
    1 1
65 AA; 7670 MW; A557395A3D527417 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 RLLCSRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----ADNGT-----GAECTTCPPGTFTLC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR006209; EGF like.
InterPro; IPR009030; Grow fac recept.
PR051TE; PS01186; EGF 2; UNKNÖWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Furin-like protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Furin-like protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 22.4%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paramecium aurelia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5889;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paramecium.
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              O9BIR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9BIR3
                                                                                                                                                                                                                                                                                                                                   Q9BIR2
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                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                        SET THE SET OF THE SET
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68 COACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHT 127
                                                                                                                                                                                                                                                                                                                                                                                                                    8 RCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECAR 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 AGDFHKKI-GLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 ASTYRSKINSSLICDMCPPGYYKNKDCTS-TSTTICLPCGEGEXTAY-NNSLTKCIRCKD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canarypox virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC VR-111;
PubMed=14671117; DOI=10.1128/JVI.78.1.353-366.2004;
PubMed=14671117; DOI=10.1128/JVI.78.1.353-366.2004;
Fulman B.R., Afconso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
J. Virol. 78:353-366(2004).
J. Virol. 78:353-366(2004).
J. Virol. 78:353-366(2004).
JRMBL; AY318871; AAR83432.1; -..
InterPro; IPR006209; GSE like.
InterPro; IPR001368; TNFR_C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 COP-----GLNRIIDNINNKCNCODGYYETTGVLACTQCSP----PCYDC
                                                                                                                                                                                                                                                                                       11.9%; Score 124; DB 2; Length 110; 21.8%; Pred. No. 0.0041; tive 19; Mismatches 51; Indels !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.9%; Score 124; DB 2; Length 117; 27.8%; Pred. No. 0.0043; ive 20; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00020; TNFR.c6; 1.
SMAR; SM00208; TNFR; 2.
PROSITE; PS01186; EGF 2; UNKNOWN 1.
PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 1.
SPGQUENCE 117 AA; 13113 MW; 06E99CAB6A41135A CRC64;
                                                                                                                                                                                                                            SEQUENCE 110 AA; 11811 MW; 5C17158141440AF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 CDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYEENEKI-FKPCNSTSDTICTCIDGYTKDETTDSCI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 RLLCSRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----ADNGT-----GAECTTCPPGTFTLC 108
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EMBL; AF351194; AAK27159.1; -.
HSSP; P12940; 1C2A.
InterPro; IPR006209; EGF like.
InterPro; IPR009030; Grow_fac_recept.
PR051TE; P801186; EGF 2; ÜNKNÖWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                  151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERM; PP0020; TNFR C6; 1.
PRINTS; PR01680; FASRECEPTOR.
SMART; SM00208; TNFR; 3.
PROSITE; PS00186; EGF 2; UNKNOWN 1.
PROSITE; PS00505; TNFR NGFR 1; 1.
PROSITE; PS50050; TNFR NGFR 1; 1.
SEQUENCE 151 AA; 17079 WW; EBAA27
                                                                                                                                                                                                                         Created)
                                                                                                                                                                             PRT;
                                                  82 ITVRNCTSTNNTVCASK 98
                         78 VALENCSAVADTRCGCK 94
                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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les 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                Q6P2H9
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                                                                                                                                 RESULT 13
                                                                                                                                                        Q6P2H9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 KIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQ 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHH 61
                                                                                                                                                                                                                                                                                                      "POLYMOTPHIAN AND TAKE THE CYCOMEGALOVITUS (CMV)-encoded tumor necrosis factor-alpha and beta-chemokine receptors in congenital CMV disease."; Infect. Dis. 186:1057-1064 (2002).

EMBL, AF498088, AAN:1057-1064 (2002).

HSSP, Q9256; LJMA.

GO: GO:0004037; F:receptor activity; IEA.

InterPro; IPR001368; TNFR.C6.

Pfam; PF00020; TNFR.C6; 1.

PROSITE; PS00050; TNFR.NGFR.1; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 GGSKM----CKPD-EVKLGNQCCPPCGSGQKVTKVCTENSG-ITCTLCPNGTYLT--GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Gaps
                                                                                                                                                                                                                                       MEDLINE=22242165; PubMed=12355354;
Arav-Boger R., Willoughby R.E., Pass R.F., Zong J.C., Jang W.J.,
Alcendor D., Hayward G.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.8%; Score 123; DB 2; Length 167; 32.3%; Pred. No. 0.0072; tive 16; Mismatches 35; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  He R., Ruan Q.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF302031; AAK60563.1; -.
HSSP; Q92956; LUWA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0004872; F:receptor activity; IEA.
Pfam; PF00020; TNFR c6; 1.
SMART; SM0208; TNFR; 2.
PROSITE; PS00552; TNFR 19: UNKNOWN 1.
PROSITE; PS50050; TNFR NGFR 1; UNKNOWN 1.
SEQUENCE 172 AA; 18911 MW; 9C9774EE9A07334C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 AA; 18339 MW; C2495E13230E9616 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human Cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                                                                                          Human cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 N--CINCTQCND--TQITVRNCTSTNNTICASK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                        Betaherpesvirinae, Cytomegalovirus.
NCBI_TaxID=10359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Conservative
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nes 30; Conserv
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                                                                                     UL144 (Fragment)
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SEQUENCE
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Mordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley D.M., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley C.M., Soarcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 LENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRDTDCG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 ccs.copcokivspcre-fretecipcgeseridtwnrethfuh----kycbpnlglrv 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 CCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFL-AW--ENHHNSECARCQACDEQASQVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, BC064518, AAH64518.1; -.. GO, GO:0016020; C:membrane; IEA. GO; GO:0016020; C:membrane; IEA. GO; GO:0004888; P:tranamembrane receptor activity; IEA. GO; GO:0006955; P:tranamembrane response; IEA. GO; GO:0007165; P:immune response; IEA. GO; GO:0007165; P:immune response; IEA. InterPro; IPR008639; Fas receptor. InterPro; IPR0080639; Fas receptor.
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: EBAA27CE7592172B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 QLGNQCCPPCKQGYRVTGQCTQ-YTSTTCTLCPNGTYVS--GLYN--CTNCTECND--TE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22242165; PubMed=12355354;
Arav-Boger R., Willoughby R.E., Pass R.F., Zong J.C., Jang W.J.,
Alcendor D., Hayward G.S.;
"Polymorphisms of the cytomegalovirus (CMV)-encoded tumor necrosis
"Polymorphisms of the cytomegalovirus (CMV)-encoded tumor necrosis
factor-alpha and beta-chemokine receptors in congenital CMV disease.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
25-OCT-2004 (TrEMBLrel. 20, Last annotation update)
25-OCT-2004 (TrEMBLrel. 20, Last annotation update)
PFTAIRE-interacting factor 2 (CG31483-PA).
Name-Pif2; Synonyms-PIF-2; ORFNames-CG31483;
Drosophila melanogaster (Fruit fly).
Bukaryota; Matazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Drosophilidae; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.7%; Score 111.5; DB 2; Length 166; 28.6%; Pred. No. 0.066; ive 20; Mismatches 28; Indels 7;
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                                                                                                                                                                                                                                                                                                                                      Human cytomegalovirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                 166 AA.
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InterPro; IPR001368; TWFR.c6.
Pfam; PF00020; TWFR.c6; 1.
SMART; SM00208; TWFR, 1.
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PROSITE; PS50050; TNFR NGFR 2; 1.
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EMBL; AF498087; AAN37946.1; -.
HSSP; Q92956; LJMA.
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                                                                 140 TCLPGF 145
                                                                                                        124 SCSPGF 129
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Addams M.D., Ceninkes S.E., 101 P.M., Newsins C.A., Googne J.D., Addams M.D., Ceninkes S.E., 110 P.M., Newsins C.A., Googne J.D., Addams M.D., Ceninkes S.E., Nole R.A., whoskins R.A., Galles R.F., Addams M.D., Ceninkes S.E., Nole R.A., whoskins R.P., Googne R.F., Genere S.E., 110 P.M., Edwag G., Chem. L.S., D. Barton G.G., Worthand J.R., Nandell N.D., Zhang G., Chem. P.F., Strong R.B., M.D., Edwag M.D., Edwag M.C., Rogers N.H., Elazel B.G., Chapter M.C., Roders M.D., Ballew M.W., Bash A., Basendale J. Barchards J. Brother M. Chandra I.D., Ballew M.W., Bash A., Basendale J. Barchards J. Brother M. Chandra I.D., Ballew M.W., Bash A., Bash M.J., Barchards J. Brother M. Chandra I.D., Ballew M.W., Bash A., Bash M.J., Barchards J. Brother M. Chandra I.D., Ballew M.W., Bash A., Barchards J. Brother M. Chandra I.D., Ballew M.W., Chandra I.D., Ballew M.W., Chandra I.D., Ballew M.W., Chandra I.D., Brother M.C., Brother M.C., Brother M.C., Brother M.D., Brother M.C., Chapter M.C., Brother M.C., Brother M.C., Brother M.C., Malden E., Courter A., Chandra I.D., Ballew M.W., Gang F., Congress J. Garg N.S., Gelbart W.M., Glasser K., Bother M.M., Garden M.P., Marchard M.C., McCang F., Congress J. Garg N.S., Gelbart W.M., Glasser K., Bother M.M., Garden M.P., McCang P., Lish Y., Harris N.L., Harris N.L., Harry D., Hallman T.J., Well M.H., Indewam C., Mallen M.W., Marchy D., Murphy D., Murphy M., Marchy M.M., Mar
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Query Match 10.5%; Score 109; DB 2; Length 118; Best Local Similarity 23.8%; Pred. No. 0.08; Matches 41; Conservative 3; Mismatches 62; Indels 66; Gaps 10;
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                                                                                                                                                                                                                                                                                                                                                                      6 SPRC-DCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSE 64
                                                                                                                                                                                                                                                                                                                                                                                                  3 SPCCGSCCGP-----CCSPC------33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 ---cspc-----cgpccspccdpccsp-----ccspccrpccrpccrpccrpccrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 LHRHTRLLCSRRDTDCGT -- CLPGFYEHGDGCVSCPTSTLGSCPERCAAVCG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----CIPCCVPCCTPCCTP-----CCTPCCSPCCGPCCSPCG 113
                                                                    FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                    (7)
SEQUENCE FROM N.A.
FlyBase SEQUENCE FROM N.A.
FlyBase SEQUENCE (WAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AF273708; AAL35411.1; -.
EMBL; AF003674; AAF54113.3; -.
HSSP; P21860; 1M6B.
FlyBase; F8900046673; Pif2.
PROSITE; PS01208; VWFC_1; UNKNOWN 1.
SEQUENCE 118 AA; 11566 MW; AFGFDISA61FF5C81 CRC64;
systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
                                              SEQUENCE FROM N.A.
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Search completed: June 27, 2005, 14:22:24 Job time : 175 secs MIS PAGE BLAMK (USPRID)

Human TRA Human TR2 Truncated

ADJ56817 AAR24083

Aar24081 Truncated Aar78612 Plasmid f Aab376228 Rat Fes r Ada49701 Extracell Aaw50286 Human Fes Ada49708 Extracell Aaw50289 Human Fes Ada49708 Extracell Aab56229 Human Fes

Abw02714 Mouse tms Ad45450 Murine tm Aar24081 Truncated Aaw5228 Truncated Ad57549 Mouse ymk Aaw82276 Truncated Aaw89238 Protein S

AAB37675 ADM46624 AABA50286 AAW50288 AAM50288 AAB4629 AAR3622 AAR3622 AAR24081 AAW52268 AAW52268 AAW52268 AAW52268 AAW52268

ALIGNMENTS

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This is the protein sequence of a mutated extracellular domain of the p55 tumour necrosis factor receptor (TNFrED) in which a Pro residue substitutes the native His-34 residue (residue 3 in the present sequence) and an Ile residue substitutes the native Ser-57 residue (residue 46 of the present sequence). Screening of TNFrED mutant clones using a yeast display system yielded a clone that showed a higher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour necrosis factor; receptor; TNFrED; proline; protein engineering; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pumour necrosis factor receptor extracellular domain H23P mutant.
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Compugen Ltd.
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                          GenCore version (c) 1993 - 2005
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Listing first 45 summaries
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length: 174
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Disclosure; Fig 16; 373pp; English

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expression level in yeast than did a wild-type TNFrED clone. The encoded polypeptide contained these 2 amino acid substitutions. The introduction of proline residues may assist the polypeptide to adopt a favourable conformation that fixes the neighbouring cysteine residue into the correct orientation for disulfide bond formation, resulting in a higher yield of correctly folded proteins in yeast or mammalian host cells. The invention therefore provides methods of increasing protein expression substituting an amino acid residue with proline, where the withins 3 maino acids of a cysteine residue. Note: The present sequence is not shown in the specification but is derived from the TNFrED sequence given in figure 4 (see ABR62363)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HODINSICCTKCPKGTYLYNDCPGPGQDTDCRECEIGSFTASENHLR-HCLSCSKCRKEM 69
                                                                                                                                                                                                                                                                                                                                                                                                                         21; Gaps
                                                                                                                                                                                                                                                                                                                                                                          19.9%; Score 206.5; DB 6; Length 161;
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les 49; Conservative
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This invention relates to an isolated nucleic acid molecule encoding a human tumour necrosis factor(TNF)-receptor related protein TR2. Included in the hiroenthon are the two splice variants of TR2. FR2-SV1 and TR2-SV2.

The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a member of the TNFR superfamily. The invention includes a method for the tragment of arthritis or inflammation using an antibody directed against a fragment of arthritis or inflammation; antianaemic, antianaemic, antialeragis, antianthritic, antiashmatic, and antibodies exhibit cytostatic, dermatological, antianaemic, antibodies exhibit cytostatic, antianaemic, antianatory, neuroprotective, nnotropic, antiashmatic, and cardiac tumours, pancreatic, breast, or prostate cancer), and immunodeficiency or for enhancing an in vivo leukocyte response to an immunodeficiency or for enhancing an in vivo leukocyte response to an immunodeficiency or for enhancing an in vivo leukocyte response to an entigen. Anti-TR2 antibodies are useful for treating, inhibiting or preventing autoimmune diseases (such as autoimmune haemolytic anaemia, dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and confined immunodeficiency (SCID) * Iniked, B cell lymphoproliferative or razagonists are useful for treating or preventing autoimmune diseases and folympetides, agonists sor antagonists are useful for treating or preventing autoimmune diseases and subibit the growth, progression and/or metastasis of cancers. They are inhibit the growth, progression and/or metastasis of cancers. They are subscuined for treating or preventing autoimmune diseases and survival, or the inhibition of apoptosis, e.g. Alzheimer's disease or treating are useful for generating antibodies are useful sease. The TR2 polypapedies are useful for generating antibodies and polypeptides and general paraeral p

as sources for generating antibodies, as molecular weight markers. This sequence represents the tumour necrosis factor receptor (TNFR) domain of the human TNFR-1 protein. The sequence was used in the characterisation of the TR2 receptor protein of the invention

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Tumour necrosis factor-receptor related protein; TR2; human; cancer; chromosome p36.2-p36.3; archritis; inflammation; autoimmune disease; immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID; severely combined immunodeficiency; apoptosis inhibition; Alzheimer's disease; Parkinson's disease; Crohn's disease.
                                                                                                                                                                                                                                                                                                                              Tumour necrosis factor receptor (TNFR) domain of TNFR-1.
                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                              29-JAN-2001
                                                                                                                                                             AAY94711;
RESULT 2
                                          AAY9471
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Homo sapiens

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99US-0126522P.
99US-0135169P.
99US-0147383P.
                                                                                    22-MAR-2000; 2000WO-US007521.
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                                                                                                                                         WPI; 2000-594519/56.
                                                                                                                NI J.
ROSEN C A.
GENTZ R L.
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                                                                  WO200056405-A2.
                                                                                            22-MAR-1999;
                                                                                                26-MAR-1999;
                                                                                                         36-AUG-1999;
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                                                                                                    20-MAY-1999
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(ROSE/)
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76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 117
                                                                                                                                                                                                                                                                                                                                                                                                               9 HPONNSICCTKCHKGTYLYNDCPGPGGDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                                                                                                                                                                                                                                   16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                             19.3%; Score 200.5; DB 3; Length 154; 29.8%; Pred. No. 1.7e-07; Live 20; Mismatches 72; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      competitive-type receptor; binding assay; cancer cell; human;
TNF receptor family; hTNFR1; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; affinity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extracellular region of human TNFR1 (hTNFR1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA49698 standard; protein; 154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  48; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                           Sequence 154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS2002192729-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA49698;
                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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19-DEC-2002.

Nucleic acid molecule encoding a human tumor necrosis factor receptor 2 and its two splice variants, useful for treating arthritis or inflammation, cancer (such as follicular lymphomas) and immunodeficiency

disorders.

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protein comprising a protein whose sequence comprises an immunogenic fragment of the amino acid residues 68-240 of the Human apoptosis inducing molecule II, AIM II, appearing as ADL17690 or a protein whose sequence comprises at least 30 or 50 amino acid residues 68-240, where the fragment comprises at least 30 or 50 amino acid residues 68-240, where the fragment comprises at least 30 or 50 amino acid residues. Also included are a hybridoma that produces the antibody, a method of detecting in a biological sample a protein that binds the antibody or its portion, a composition comprising the antibody and a carrier and an isolated cell that produces the antibody. Human AIM II is a member of the tumour necrosis ligand superfamily and has been shown to bind lymphotoxin-beta receptor and TR6 (TRAIL receptor 6). The antibody is useful for preparing a composition for treating e.g., lymphadenopathy, aberrant bone development, autoimmune disease, graft-versus-host disease, rheumatoid arthritis, osteoarthritis or cancer (many other disease, and conditions are listed in the specification). The present sequence represents a cysteine-rich motif from a protein thought to bind AIM II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein, useful for preparing a composition for treating e.g.,
lymphadenopathy, autoimmune disease, rheumatoid arthritis, osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated antibody or its portion binding to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibody that binds to human Apoptosis Inducing Molecule II (AIM II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.3%; Score 200.5; DB 7; Length 154; 29.8%; Pred. No. 1.7e-07; Live 20; Mismatches 72; Indels 21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ebner R, Yu G, Ruben SM, Ullrich S, Zhai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 13; SEQ ID NO 53; 163pp; English.
                                                                        960S-0030157P.
970S-00822953.
980S-0003886.
980S-00027287.
990S-00252656.
                                                                                                                                                                                                                                                               99US-0137457P.
99US-0142657P.
99US-0148326P.
99US-0168380P.
10-MAR-2000; 2000US-00523323
                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-810570/76.
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Best Local Similarity
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                                                                                                                                   07-JAN-1998
                                                                                                                                                                                      20-FEB-1998;
                                                                                                                                                                                                                                        11-MAR-1999
                                                                                                                                                                                                                                                                       04-JUN-1999
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                                                                                                       21-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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ADJ56814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to the isolation of a biologically active Apo-2 ligand inhibitor (Apo-2LI) or Apo-3, and the polymucleotide sequences encoding them. Apo-2LI and Apo-3 are involved in apoptosis. The Apo-2LI and Apo-3 polypeptides are useful in diagnostic assays. Apo-2LI is useful for generating antibodies, as standards in assays for Apo-2LI in affairty purification techniques, and in competitive-type receptor binding assays when labelled with radioiodine, enzymes or fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or inducing apoptosis in cancer cells, and thus have therapeutic utility. The present sequence represents the extracellular region of a human TNF receptor family protein. This sequence is compared with the extracellular region of human Apo-2LI.
                                                                                                                                                                                                                                                                                                                                        Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or Apo-3 polypeptide which induces or stimulates apoptotic activity, useful in diagnostic assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; apoptosis inducing molecule II; AIM II; antibody; tumour necrosis ligand superfamily; lymphotoxin-bera receptor; TR6; TRAIL receptor 6; lymphadenopathy; aberrant bone development; autoimmune disease; graft-versus-host disease; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.3%; Score 200.5; DB 6; Length 154; 29.8%; Pred. No. 1.7e-07; tive 20; Mismatches 72; Indels 21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADL17741 standard; protein; 154 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2; 53pp; English.
                      28-MAR-2002; 2002US-00112793.
                                                                           96US-00625328.
                                                                                                     96US-00710802.
97US-00828683.
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                                                                                                                                                                                                                                                                                        WPI; 2003-657226/62
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                                                                                                                                                                                                                                      Ashkenazi AJ;
                                                                              01-APR-1996;
                                                                                                     23-SEP-1996;
31-MAR-1997;
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Query Match Matches

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7;

21;

75 63

ADJ56814 standard; protein; 154 AA

Homo sapiens US6635743-B1

118

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RESULT 4

ADL17741;

21-OCT-2003

06-MAY-2004 (first entry)

ADJ56814;

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133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
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                                                                                                                                                                          ABG74752;
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AC AAR2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to apoptosis inducing molecule II (AIM III), a TNF (tumour necrosis factor)-ligand superfamily member and its corresponding nucleic acid sequence. The invention is useful for preventing, treating, ameliorating, diagnosing or prognosing graft versus host disease, immunodeficiency, cancer, autoimmune diseases such as multiple sclerosis, type I diabetes, rheumatoid arthritis, primary biliary cirrhosis, aplastic ansemia, myelodysplasia, systemic lupus erythematosus and idiopathic thrombocytopenic purpura. It is useful for screening or identifying compounds capable of enhancing or inhibiting cellular response induced by AIM II, for inhibiting, blocking or reducing T-cell activation. AIM II is useful as a molecular weight marker on SDS-PAGE gels or on gel filtration columns. The present sequence is a cysteinerich motif of human TNF receptor (TNFR) family member.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated apoptosis inducing molecule II polypeptide, useful for treating, preventing, ameliorating, diagnosing or prognosing autoimmune diseases such as multiple sclerosis, rheumatoid arthritis, aplastic anemia.
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                                 Apoptosis inducing molecule II; AlM II; TNF; tumour necrosis factor; therapy; graft versus host disease; immunodeficiency; cancer; autoimmune disease; multiple sclerosis; type I diabetes; rheumatoid arthritis; primary bilary cirrhosis; aplastic anaemia; myelodysplasia; systemic lupus erythematosus; didiopathic thrombocytopenic purpura; cellular response; T-cell activation; molecular weight marker; human; TNF receptor; TNFR.
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19.3%; Score 200.5; DB 8; Length 154;
Best Local Similarity 29.8%; Pred. No. 1.7e-07;
Matches 48; Conservative 20; Mismatches 72; Indels 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ullrich S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 13; SEQ ID NO 53; 189pp; English
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Human TNFR-I cysteine-rich motif.
                                                                                                                                                                                                                                                                                                                                        96US-0013923P.
96US-0030157P.
98US-0002388.
98US-00027287.
98US-00252656.
99US-0124041P.
99US-0124041P.
99US-0143427P.
99US-0148326P.
99US-0148326P.
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07-JAN-1998;
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76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel polynucleotide sequences encoding tumour necrosis factor (TNF) receptor (TNF-R) or TNF binding protein (TNF-BP). The products of the invention are useful in pharmaceutical compositions for prophylaxis or treatment of human tumours and to understand the mechanisms of TNF action. This sequence represents a fragment of the TNF-BP described in the disclosure of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 155
118 EKONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding TNF binding protein and TNF- receptor -
treatment and to understand mechanisms to TNF action.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stratowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.3%; Score 200.5; DB 329.8%; Pred. No. 1.8e-07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maurerfogy I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BOEH ) BOEHRINGER INGELHEIM INT GMBH
                                                                                                                                                                             Ź
                                                                                                                                                                                                                                                                                                                                                        Human TNF binding protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR27496 standard; protein; 161 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 23; Page 34; 51pp; German.
                                                                                                                                                                       ABG74752 standard; protein; 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90EP-00106624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89DE-03913101
89DE-03920282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Himmler A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SYND ) SYNERGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1990-321987/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hauptmann R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-1989;
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GQVEISSCTVDRDTVCGCRRNQYRHYWSENLFQC-----FNCSLCLN-GTVH----LSCQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soluble tumour necrosis factor receptor; sTNFR; TNF-mediated disease; tumour necrosis factor binding protein; autoimmune disease; arthritis; adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy; chronic fatigue syndrome; graft rejection; Alzheimer's disease; TNBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treatment of acute or chronic inflammatory disease, e.g. leukaemia - by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the amino acid sequence of the human tumour necrosis factor receptor type I, used in the method of the invention involving the treatment of acute or chronic inflammatory disease such as leukaemia by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.3%; Score 200.5; DB 2; Length 161; 29.8%; Pred. No. 1.8e-07; Live 20; Mismatches 72; Indels 21
                                                            Human; tumour necrosis factor; TNF; TNF receptor type I; inflammatory disease; leukaemia; TNF binding protein; anti-inflammatory drug; methotrexatess.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 155
                         Human soluble tumour necrosis factor receptor type I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soluble tumour necrosis factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Edwards CK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 1, 104pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW52267 standard; protein; 161
                                                                                                                                                                                                                                                                                                                                96US-0032587P.
97US-0036355P.
97US-0039315P.
97US-0052023P.
                                                                                                                                                                                                                                                                                           97WO-US022733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sennello RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-333039/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV41548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bendele AM,
                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                   WO9824463-A2
                                                                                                                                                                                                                                                                                           38-DEC-1997;
                                                                                                                                                                                                                                                                                                                                     06-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUN-1998
                                                                                                                                                                                                                                               11-JUN-1998
                                                                                                                                                                                                                                                                                                                                                            23-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
    셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New ethylene! glycolated polypeptide(s) with improved pharmacokinetic properties - for treating e.g. TNF and IL-1 mediated diseases, e.g. adult respiratory distress syndrome, rheumatoid arthritis, septic shock etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence shows a native 30 kD TNF inhibitor which may be modified to contain at least one non-native cysteine residue, pref. at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is joined to a non-peptidic polymer, pref. monomethoxy PEG via thio-ether bonds. Two such TNF inhibitor mols may be linked via this non-peptidic spacer. The modified polypeptides show improved pharmokinetic properties, i.e. increased mol. w. hence reduced clearance rate following s.c. or systemic administration, increased sol. of native TNF inhibitors, and reduced antigenicity. The polypeptides may be used for treatment of TNF mediated diseases such as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid arthritis, inflammatory bowel disease and septic shock. The same method may be applied to the interleukin-1 receptor antigonist IL-1ra. See also AAR27495. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 HPONNSICCTKCHKGTYLYNDCPGPGODTDCRECESGSFTASENHLR-HCLSCSKCRKEM 69
                                                                                                        Tumour necrosis factor; ethylene glycol; pharmokinetic; adult respiratory distress syndrome; rheumatoid arthritis; septic shock; pulmonary fibrosis; spacer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.3%; Score 200.5; DB 2; Length 161; larity 29.8%; Pred. No. 1.8e-07; Conservative 20; Mismatches 72; Indels 21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kohno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brewer MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evans RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 54; Fig 2; 100pp; English.
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                                                                                                                                                                                                                                                                                                                                     92WO-US002122.
                                                                                                                                                                                                                                                                                                                                                                             91US-00669862.
                    (first entry)
                                                              Native 30 kD TNF inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Armes LG,
  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYND ) SYNERGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1992-348933/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thompson RC,
                                                                                                                                                                                                                                                                                                                                                                               15-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                    17-JAN-1992;
                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                             W09216221-A1
25-MAR-2003
09-MAR-1993
                                                                                                                                                                                                                                                                                         01-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48;
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Gaps

21;

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AAW59664;

RESULT 8 AAW59664

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OPG; chimeric; fusion; dimerisation domain; autoimmune disease;
                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 92pp; English.
                                                                                                                   98WO-US008631.
                                                                                                                                           97US-00850188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human 30 kDa TNF inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
             inflammation; apoptosis.
                                                                                                                                                                                               Soyle WJ, Wooden S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                       WPI; 1999-034661/03
                                                                                                                                                                     (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                    N-PSDB; AAV81732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 161 AA;
                                                                                                                  29-APR-1998;
                                                                                                                                           01-MAY-1997;
                                        Homo sapiens
                                                                409849305-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB37676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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AAB37676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is the human soluble tumour necrosis factor receptor (STNFR). The protein was used to make the truncated sTNFR proteins of the invention. The truncated sTNFR proteins and tumour necrosis factor binding proteins (TNBP) are used to treat any TNF-mediated disease, e.g. arthritis, adult respiratory distress syndrome, cachexia/anorexia, cancer, chronic fatigue syndrome, graft rejection, Alrahemer's diseases and other autoimmune diseases. Cells transformed with a vector containing blw encoding the protein may be used for production of recombinant sTNFR, which may also be used for measuring the amount of sTNFR; in samples and to raise antibodies against sTNFR. TNPR may also be used in preparation of therapeutic compositions for treating the above diseases. The sTNFR deamidation site in region 111-126, so are more stable in vivo); contain fewer disulphide bonds and fewer epitopes, making them less antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 69
                                                                                                                                                                                                                                                                       Iruncated and soluble forms of tumour necrosis factor receptor - useful for treating diseases involving factor, e.g. arthritis and adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 19.3%; Score 200.5; DB 2; Best Local Similarity 29.8%; Pred. No. 1.8e-07; Matches 48; Conservative 20; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour necrosis inhibitor 30 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW89233 standard; protein; 161 AA
                                                                                                                                                                                                           Kieft GL;
                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1; 205pp; English
                                                                                                                 96US-0032534P.
97US-0037737P.
97US-0039314P.
97US-0039792P.
                                                                                                                                                                                                                                                                                   for treating diseases involvir
respiratory distress syndrome.
                                                                           97WO-US012244
                                                                                                    96US-0021443P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   than full-length proteins
                                                                                                                                                                                                         Edwards CK,
                                                                                                                                                                                                                                  WPI; 1998-101052/09.
                                                                                                                                                                                 (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                               N-PSDB; AAV19801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 161 AA;
 Homo sapiens
                         WO9801555-A2
                                                                           09-JUL-1997;
                                                                                                                                                        04-MAR-1997;
                                                   15-JAN-1998
                                                                                                    09-JUL-1996
                                                                                                                              23-JAN-1997,
07-FEB-1997,
                                                                                                                                                                                                         Fisher EF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW89233;
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ID AAW8
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AC AAW8
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DT 04-M
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YW TUMC
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The present invention describes a chimeric polypeptide (A1), comprising an osteoprocegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated A1 monomers; (2) an isolated nucleic acid encoding A1; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are used to treat TNF and TNFR—mediated disorders such as inflammation, used to treat TNF and TNFR—mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with the fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents the TNF inhibitor 30 kDa protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 GOVEISSCTVDRDTVCGCRKNOYRHYWSENLFOC----FNCSLCLN-GTVH----LSCO 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New chimeric osteoprotegerin polypeptides - contain the osteoprotegerin dimerisation domain and a heterologous sequence, useful to treat TNF and TNFR-mediated disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin; IL-1; inflammatory disease; degenerative disease; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE -- RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.3%; Score 200.5; DB 2 29.8%; Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB37676 standard; protein; 161 AA
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The present sequence is the protein sequence of the extracellular domain of the p55 tumour necrosis factor receptor (TMPRED). Screening of TNEED mutant clones using a yeast display system yielded 2 mutant clones (see AR862364 and ABR62365) that showed higher expression levels in yeast than in wild-type TNFrED. The first clone contained a proline residue that substituted the native Ser-87 residue (Dosition 76 of the present sequence). The other clone contain a proline residue that substituted the native His-34 residue (13 of the present sequence) and also an isoleucine native His-34 residue (23 of the present sequence) and also an isoleucine sequence) of TNFrED. The invention provides methods of increasing protein sequence) of TNFrED. The invention provides methods of increasing protein captured the substituting an amino acid residue with proline, where the substitution occurs within 10, and captorial sessions may assist the polypeptide to adopt a favourable conformation that fixes the neighbouring cysteine residue into the correct orientation for disulfide bond formation, resulting in a higher yield of correctly folded proteins in yeast or mammalian host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
                                                                                                                                                                                                                                                                                                                                                                                                     Increasing expression of a protein, comprises substituting at least one codon in the polynucleotide encoding the protein, for a codon encoding proline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 SQVALENCSAVADTRCGCKPGWFVEC --- QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
/note= "corresponds to wild-type Ser57 residue" Misc-difference 76 /note= "corresponds to wild-type Ser87 residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; tumour necrosis factor inhibitor; 30kDa TNF inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6; Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 EKONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 RRDIDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.3%; Score 200.5; DB 6; 29.8%; Pred. No. 1.8e-07; tive 20; Mismatches 72;
                                                                                                                                                                                                                                                         (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
                                                                                                                                                                                                                                                                                                  Schweickhardt RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA20577 standard; protein; 161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human 30kDa TNF inhibitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 4; 53pp; English.
                                                                                                                                                                                                                    30-NOV-2001; 2001US-0340648P.
                                                                                                                                                                          21-NOV-2002; 2002WO-EP013059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Matches 48; Conservative
                                                                                                                                                                                                                                                                                                  Brondyk W, Jiang X,
                                                                                                                                                                                                                                                                                                                                            WPI; 2003-523245/49
                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ACC84134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 161 AA;
                                                                                         WO2003046160-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-2003
                                                                                                                                 05-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to Tumour Necrosis Factor (TNF) inhibitors (see AAB37676 and AAB37685), which have TNF inhibitory activity. The novel TNF inhibitors of the present invention are useful as therapeutic agents for inhibiting the activity of TNF and interleukin (IL-1), and for treating inflammatory and degenerative diseases mediated by TNF. The 30 kba TNF inhibitor can inhibit TNF alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel 30 kDa tumor necrosis factor inhibitor analog comprising a non-native cysteine residue cross-linked with polyethylene glycol, useful for treating inflammatory and degenerative diseases mediated by TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "corresponds to wild-type His34 residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumour necrosis factor; receptor; proline; protein engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.3%; Score 200.5; DB 4; Length 161; 29.8%; Pred. No. 1.8e-07; ive 20; Mismatches 72; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                  Thompson RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour necrosis factor receptor extracellular domain.
                                                                                                                                                                                                                                                                                                                                                                King MW, Hale KK, Brewer MT, RW, Vannice J, Kohno T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABR62363 standard; protein; 161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 19; 82pp; English
                                                                                                                                                                                                               89US-00450329.
90US-00479661.
90US-00555274.
                                                                                                                                                    95US-00375242
                                                                                                                                                                                            89US-00381080
                                                                                                                                                                                                                                                                               93US-00090366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               2001-006443/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                      (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAC83945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                        Vanderslice RW,
                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                    19-JAN-1995;
                                                                                                                                                                                                                                                                               09-JUL-1993;
                                                                   US6143866-A
                                                                                                                                                                                                                 11-DEC-1989;
07-FEB-1990;
                                                                                                                                                                                              18-JUL-1989
                                                                                                             07-NOV-2000
                                                                                                                                                                                                                                                             19-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                    Squires C,
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WO2003104263-A2
                                                              11-DEC-1989;
07-FEB-1990;
19-JAN-1995;
                                 07-JUN-1995;
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                                                      18-JUL-1989
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                                                                                                                                                                                                                                                                                                                                                                                                           48;
             01-APR-2003
                                                                                                                             Brewer MT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                    The present invention relates to the isolation of novel human tumour necrosis factor (TNF) inhibitor polypeptides (designated 30kDa TNF inhibitor and 40kDa TNF inhibitor), and the polymucleotide sequences encoding them. Also disclosed is a fragment of the 30kDa TNF inhibitor polypeptide which comprises at least one non-native cysteine residue at the N-terminus, C-terminus, residue 14 or preferably 105. The polymucleotide sequence encoding the 30kDa TNF inhibitor is useful for manufacturing a medicament for treating a pathological condition mediated by TNF. The present sequence represents human 30kDa TNF inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQVALENCSAVADTRCGCKPGWFVEC -- QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
                                                                                                                                                                                                                        New nucleic acid comprising a sequence that encodes a polypeptide having TNF inhibitory activity, useful for manufacturing a medicament for treating a pathological condition mediated by TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, tumour necrosis factor inhibitor, 30kDa TNF inhibitor, 40kDa TNF inhibitor, TNF mediated pathological condition.
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6; Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
40kDa TNF inhibitor; TNF mediated pathological condition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 EKQNTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 155
                                                                                                                                                                                                                                                                                                                                                                                                                             19.3%; Score 200.5; DB 6; 29.8%; Pred. No. 1.8e-07; tive 20; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA20579 standard; protein; 161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human 30kDa TNF inhibitor protein.
                                                                                                                                                                                                                                                                   Example 2; Fig 19; 85pp; English.
                                                                                                                                                                                 Kohno
                                                                                                       89US-00381080.
89US-00450329.
90US-00479661.
95US-00375242.
                                                                                   95US-00484337.
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                                                                                                                                                                                Thompson RC,
                                                                                                                                                                                                     WPI; 2003-531100/50.
                                                                                                                                                           (ANGE-) ANGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 161 AA;
                                                                                                                 11-DEC-1989;
07-FEB-1990;
19-JAN-1995;
                      Homo sapiens
                                          JS6541620-B1
                                                                                  07-JUN-1995;
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                                                               01-APR-2003
                                                                                                                                                                               Brewer MT,
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
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                                                                                                                                                                                                                                                                                                                                                                                     protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid comprising a sequence that encodes a polypeptide having TNF inhibitory activity, useful for manufacturing a medicament for treating a pathological condition mediated by TNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human tumour necrosis factor receptor 1 (TNF-R1) protein, SEQ ID No 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 RRDIDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
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                                                                                                                                                                                                                                                                                                                                      Kohno T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 20; 85pp; English.
                                                                  89US-00381080.
89US-00450329.
90US-00479661.
95US-00375242.
95US-00484337.
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                                                                                                                                                                                                                                                                                                                                      Thompson RC,
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                                                                                                                                                                                                                                                           (ANGE-) ANGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADA20578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 161 AA;
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26-FEB-2003; 2003WO-US005917.
         01-MAY-2002; 2002US-0376743P.
                (GEMV ) GENENCOR INT INC.
                       Power SD;
                              WPI; 2004-062306/06.
                       Harding FA,
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Determining T-cell epitope of a protein (e.g. cytokine or cytokine receptor), useful for reducing protein allergenicity, comprises combining differentiated dendritic cells and naive T-cells with a peptide having The invention relates to a novel method for determining a T-cell epitope of a protein, where the protein is selected from cytokines and cytokine receptors. The method comprises combining a solution of differentiated dendritic cells and naive CD4+ and/or CD8+ T-cells with a pepset of peptides comprising the T-cell epitope. The composition and methods are useful in reducing the immunogenicity of cytokines and cytokine receptors such as interferon-beta, soluble tumour necrosis factor receptor-1, erythropoietin or thrombopoietin. These modified cytokines and cytokine receptors may be used for treating various conditions such as inflammation, cancer or anaemia. This sequence represents the human tumour necrosis factor receptor 1 (TNF-R1) protein of the invention. Claim 4; SEQ ID NO 106; 51pp; English. the T-cell epitope.

Sequence 161 AA;

7; 70 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 119 76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132 11 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 69 16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 75 Query Match
19.3%; Score 200.5; DB 8; Length 161;
Best Local Similarity 29.8%; Pred. No. 1.8e-07;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171 g ઠે 요 ð 8

Search completed: June 27, 2005, 14:18:38 Job time : 163 secs

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76 SQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDC--GALHRHTRLLCSR
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Sequence 422, App
Sequence 13, Appl
Sequence 20, Appl
Sequence 423, App
Sequence 410, Appl
Sequence 11, Appl
                                                                                                                                                                                                                                               June 27, 2005, 14:19:32 ; Search time 158 Seconds (without alignments) 423.490 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16,
Sequence 19,
Sequence 21,
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1 QGGTRSPRCDCAGDFHKKIG......CPTSTLGSCPERCAAVCGWR 174
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1: /cgn2 6/ptodata///pubpaa/USO7 PUBCONB.pep:*
2: /cgn2 6/ptodata///pubpaa/PCT_NEW PUB.pep:*
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5.1.6
Compugen Ltd.
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1 US-10-218-102-422

US-09-798-789-13

US-09-798-789-20

4 US-10-218-102-423

4 US-10-218-102-423

US-10-218-102-421

US-09-798-789-11

US-09-899-423A-16

US-09-798-789-19

US-09-798-789-19
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GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-081-280-6_COPY_25_198
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Match Length
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seq length: 174
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Sequence 53, Appli
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Sequence 4, Appli
Sequence 10, Appl
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Sequence 17, Appl
Sequence 427, App
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Fatent No. US200200978041

GENERAL INFORMATION:

APPLICANT: Palikov, Anton

TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA

TITLE OF INVENTION: DISCREERS

TITLE OF INVENTION: DISCREERS

TITLE OF INVENTION: DISCREERS

FILE REFERENCE: A-68990-1/RFT/RMS/RMK

CURRENT APPLICATION NUMBER: US/09/798, 789

CURRENT PAPLICATION NUMBER: US 60/186,427

PRIOR PILING DATE: 2000-03-02

PRIOR PILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PATENTIN VET: 2.1

SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-798-789-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.3%; Score 210.5; DB 9; Length 162; 30.0%; Pred. No. 2.6e-09; Live 20; Mismatches 73; Indels 19;
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Query Match 20.3%
Best Local Similarity 30.0%
Matches 48; Conservative
RESULT 1
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US-10-218-102-423
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US-09-798-789-20
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76 SQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDC--GALHRHTRLLCSR 133
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                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bentzien, Joerg
APPLICANT: Bentzien, Joerg
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Hayes, Robert J.
APPLICANT: Hayes, Robert J.
APPLICANT: Vielmetter, Jost
ITLE OF INVENTION: Protein Design Automation for Protein Libraries
FILE REFERENCE: A-6722-11/FT/RNS/RMX
CURRENT APPLICATION NUMBER: US/10/218,102
FURNENT APPLICATION NUMBER: US 09/927,790
PRIOR APPLICATION NUMBER: US 09/927,790
PRIOR PILING DATE: 2001-09-10
PRIOR PELING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US 60/311,545
PRIOR APPLICATION NUMBER: US 60/311,937
PRIOR APPLICATION NUMBER: US 60/351,937
PRIOR APPLICATION NUMBER: US 60/351,937
PRIOR APPLICATION NUMBER: US 60/351,937
PRIOR APPLICATION NUMBER: US 60/352,103
PRIOR PILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 432
SOFTWARE: PatentIn version 3.1
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Fatent No. US2002009780A1
GENERAL INFORMATION:
APPLICANT: Dahiyat, Bassil
APPLICANT: Filikov, Anton
TITLE OF INVENTION: DASIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
TITLE OF INVENTION: DASIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
TITLE OF INVENTION: DISORDERS
TITLE OF INVENTION: DISORDERS
TITLE OF INVENTION: DISORDERS
TITLE OF INVENTION DISORDERS
TILE REFERENCE: A-68990-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/798,789
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,427
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                                                                                                                      122 KONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 RDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
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                                                                                                                                                                                                                                                               Sequence 422, Application US/10218102
Publication No. US20030130827A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) OTHER INFORMATION: synthetic US-10-218-102-422
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Best Local Similarity
Matches 48; Conserv
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US-09-798-789-13
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71 GQVEISSCTVDRDTVCGCRRNQYRHYQSENLFQC-----FNCSLCLN-GTVH-----LSCQ 120
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APPLICANT: Dahiyat, Anton
TITLE OF INVENTION: DESIGNAND DISCOVERY OF PROTEIN BASED TNF-ALPHA
TITLE OF INVENTION: DESIGNAND DISCOVERY OF THE TREATMENT OF TNF-ALPHA TITLE OF INVENTION: DISCREBES
FILE REPERENCE: 4-68990-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US(09/798,789
PRIOR APPLICATION NUMBER: US 60/186,427
PRIOR PILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 20
LENGTH: 162
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                                                                                                                                                                                                                                                                                                                                               Query Match
19.8%; Score 205.5; DB 9; Length 162;
Best Local Similarity 30.0%; Pred. No. 6.5e-09;
Matches 48; Conservative 19; Mismatches 74; Indels 19
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PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 162
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SOFTWARE: PatentIn version 3.1
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US-10-218-102-421
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                                               SEQ ID NO 430
LENGTH: 162
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         GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Deliyat, Bobert J.
APPLICANT: Hayes, Robert J.
APPLICANT: Vielmetter, Jost
TILE OF INVENTION: Protein Delign Automation for Protein Libraries
FILE REFERENCE: A-6722-11/RFYRMS/RMK
CURRENT APPLICATION NUMBER: US/10/218,102
FURRENT APPLICATION NUMBER: US 69/927,790
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
PRIOR PLING DATE: 2001-09-25
PRIOR FILING DATE: 2002-01-25
PRIOR PRIOR DATE: 2002-01-25
PRIOR PRIOR DATE: 2002-01-25
PRIOR PLING DATE: 2002-01-25
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APPLICANT: Bentzien, Joerg
APPLICANT: Bentzien, Joerg
APPLICANT: Bentzien, John R.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Hayes, Robert J.
APPLICANT: Hayes, Robert J.
APPLICANT: Vielmetter, Jost
TITLE OF INVENTION: Protein Design Automation for Protein Libraries
FILE REFERENCE: A-67229-11/FRF/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/218,102
FRIOR APPLICATION NUMBER: US 09/927,790
FRIOR PILING DATE: 2001-08-10
FRIOR PILING DATE: 2001-09-10
FRIOR PILING DATE: 2001-09-25
FRIOR APPLICATION NUMBER: US 60/324,899
FRIOR APPLICATION NUMBER: US 60/321,937
FRIOR PILING DATE: 2002-01-25
FRIOR PILING DATE: 2002-01-25
FRIOR FILING DATE: 2002-01-25
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Publication No. US20030130827A1
GENERAL INFORMATION:
Publication No. US20030130827A1
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US-10-218-102-423
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76 SQVALENCSAVADTRCGCKPGWFVECQ---VSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
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Patent No. US2002009780A1

GENERAL INFORMATION:

APPLICANT: Dahiyat, Bassil

TITLE OF INVENTION: UNRANTS FOR THE TREATMENT OF TNF-ALPHA RELATED

TITLE OF INVENTION: USCREBES

FILE REFERENCE: A-68900-1/RFT/RMS/RMK

CURRENT FILING DATE: 2001-03-02

PRIOR PLING DATE: 2001-03-02

RUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.1

SEMENT: APPLICATION OF THE TREATMENT OF THE TRE
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US-09-798-789-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 19.6%; Score 203.5; DB 9; Length 162; Best Local Similarity 30.0%; Pred. No. 9.3e-09; Matches 48; Conservative 19; Mismatches 74; Indels 19;
                                                                                                                                                                                                                                                                                                                                Query Match 19.8%; Score 205.5; DB 14; Length Best Local Similarity 30.4%; Pred. No. 6.5e-09; Matches 49; Conservative 20; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
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Publication No. US20030130827A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                         ; OTHER INFORMATION: synthetic US-10-218-102-430
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us-10-081-280-6_copy_25_198.rapb

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US-09-798-789-19
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US-09-798-789-21
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APPLICANT: Himmler, Adolph
APPLICANT: Himmler, Adolph
APPLICANT: Himmler, Adolph
APPLICANT: Stratowa, Christian
ITILE OF INVENTION: TWE Receptors, TWF Binding Proteins and DNAs Coding for
ITILE OF INVENTION: TWE
ITILE OF INVENTION: TWE
ITILE OF INVENTION: TWE
CURRENT APPLICATION NUMBER: 08/99,429A
CURRENT FILING DATE: 2001-07-03
FRIOR APPLICATION NUMBER: 08/779,356
FRIOR PILING DATE: 1925-06-07
FRIOR APPLICATION NUMBER: 08/477,639
FRIOR PILING DATE: 1995-00-01
FRIOR APPLICATION NUMBER: 08/153,287
FRIOR APPLICATION NUMBER: 08/153,287
FRIOR PILING DATE: 1993-11-17
FRIOR PILING DATE: 1993-11-17
FRIOR PILING DATE: 1993-01-02
FRIOR PILING DATE: 1993-01-02
FRIOR FILING DATE: 1992-01-02
FRIOR FILING DATE: 1990-04-20
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APPLICANT: Bentzien, Joerg
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Hayes, Robert J.
TITLE OF INVENTION: Protein Design Automation for Protein Libraries
FILE REFERENCE: 2002-08-12
CURRENT APPLICATION NUMBER: US 09/927,790
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR PLICANION NUMBER: US 60/311,545
PRIOR PLICATION NUMBER: US 60/324,899
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2002-01-25
SOFTWARE: Patentin version 3.1
SEQ ID NO 421
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ORGANISM: Artificial Sequence
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APPLICANT: Himmler, Adolph
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Matches 48; Conservative
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60 HHNSECARCQACDEQASQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQP 116
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                                                                                                                                                                                                                                                                                                                      3 GTRSPR---CDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWEN 59
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                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: recombinant; OTHER INFORMATION: TNR-BP sequence
US-09-899-429A-16
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                                                                                                                                                                                                                               Length 173;
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                                                                                                                                                                                                                          Query Match 19.6%; Score 203; DB 9; Best Local Similarity 29.4%; Pred. No. 1.1e-08; Matches 52; Conservative 20; Mismatches 81;
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                                                                  TYPE: PRT ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 173
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71 GQVEISSCTVDRDTVCGCRKNQYRHYKSENLFQC----FNCSLCLN-GTVH----LSCQ 120
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US-10-218-10
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                                                                                                                                                                    12 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM
                                                                                                              16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
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                                         Gaps
                                         21;
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Best Local Similarity 29.8%; Pred. No. 1.3e-08;
Matches 48; Conservative 21; Mismatches 71; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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                        APPLICANT: Dahlyat, Bassil
APPLICANT: Dahlyat, Bassil
APPLICANT: Filkov, Anton
TITLE OF INVENTION: DESIGN AND DISCOVERY OF PROTEIN BASED TNF-ALPHA
TITLE OF INVENTION: UARIANTS FOR THE TREATMENT OF TNF-ALPHA RELATED
FILE REFERENCE: A-68990-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/798,789
CURRENT FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/186,427
PRIOR APPLICATION NUMBER: US 60/186,427
PRIOR PILING DATE: 2000-03-02
SOFTWARE: PATENTIN VOS: 2.1
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APPLICANT: Bentzien, John R.
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Desjarlais, John R.
APPLICANT: Hayes, Robert J.
APPLICANT: Vielmetter, Jost
TITLE OF INVENTION: Protein Design Automation for Protein Libraries
FILE REFERENCE: A-67229-11/RFT/RMS/RMK
CURRENT APPLICATION NURSE: U5/10/218,102
CURRENT FILING DATE: 2002-08-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: synthetic US-09-798-789-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 19.4%; Score 201.5; DB 9; Length 162; Best Local Similarity 29.8%; Pred. No. 1.3e-08; Matches 48; Conservative 20; Mismatches 72; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 EKQNTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 156
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PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-25
PRIOR FILING DATE: 2002-09-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
NUMBER OF SEQ ID NOS: 432
SSOTTWARE: PALENTIN VETSION 3.1
SSOTTWARE: PALENTIN VETSION 3.1
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Publication No. US20030130827A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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US-10-218-102-429
GENERAL INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/800,909
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-638-5197
TELEPHONE: 202-737-3528
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                  APPLICANT: BELETSKY, IGOR
APPLICANT: BRITY, IGOR
APPLICANT: BNGELMANN, HATUMUT
TITLE OF INVENTION: TW INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESCONDENCE ADDRESS:
ADDRESSEE: BROWNY AND NEIMARK
                                                                                                                                                                                                                                                                          ADDRESSEE: BROWDY AND NEIMARK STREET: 419 Seventh Street, N.W. CITY: Washington STATE: D.C.
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
NAME:
BROWDY, ROGER L.
BROSENER DATE:
BROWDY, ROGER L.
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BROWDY, ROGER L.
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APPLICATION NUMBER: 08/476,862
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TYPE: amino acid
STRANDEDNESS: single
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US-09-884-987-4
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FILE DEFINATION: DNA CODING FOR HUMAN CELL SURFACE ANTIGEN
FILE REPRENCE: 0020-4877P
CURRENT APPLICATION NUMBER: US/09/884,987
CURRENT FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 4
LENGTH: 153
TYPE: PRT
COGANISM: Homo sapiens
US-09-884-987-4
QUELY MATCH
BEST Local Similarity 29-8%; Pred. No. 1.5e-08;
MATCHES A8; Conservative 20; Mismatches 72; Indels 21; Gaps 7
COGANISM: Homo sapiens
US-09-884-987-4
QUELY MATCH
COMMISM: PRED. Pred. No. 1.5e-08;
MATCHES A8; CONSERVATIVE 20; Mismatches 72; Indels 21; Gaps 7
COGANISM: PRED. PRED. PRED. Indels 21; Gaps 7
COMMISM: PRED. PRED. Indels 21; Gaps 7
COMMISM: Indels 21; COMMISM: Indels 21; Gaps 7
COMMISM: Indels 21; COMMISM: Indels 21; Gaps 7
COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMISM: Indels 21; COMMI
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Best Local Similarity
Matches 48; Conservat
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Sequence 3, Appl
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                                                                 June 27, 2005, 14:15:57; Search time 42 Seconds (without alignments) 309.260 Million cell updates/sec
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                                                                                                                              1 QGGTRSPRCDCAGDFHKKIG......CPTSTLGSCPERCAAVCGWR 174
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Sequence 12
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1: /cgn2 6/ptodarcal/iaa/5A COMB.pep:*

2: /cgn2 6/ptodarcal/iaa/5B COMB.pep:*

3: /cgn2 6/ptodatcal/iaa/6A_COMB.pep:*

4: /cgn2 6/ptodatcal/iaa/6B_COMB.pep:*

5: /cgn2 6/ptodatcal/iaa/PCTUS COMB.pep:*

6: /cgn2 6/ptodatcal/iaa/PCTUS COMB.pep:*
        5.1.6
Compugen Ltd.
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US-09-523-323-53
US-09-326-394-2
US-08-232-087A-10
US-08-766-945D-129
US-09-855-266A-13
US-09-146-950-4
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US-09-52-31-35-56

US-08-050-319B-54

US-08-465-982-54

US-09-41-722-2

US-09-855-266A-2

US-09-815-237B-3
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US-08-468-560C-4
US-09-800-909-3
US-09-800-908-12
                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-828-683A-15
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US-09-180-100-9
                                                                                                                                                                                 513545 segs, 74649064 residues
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        GenCore version
Copyright (c) 1993 - 2005
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Listing first 45 summaries
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length: 174
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Perfect score:
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APPLICANT: ING, Naoto
APPLICANT: TOH, Naoto
APPLICANT: TOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: ADDRESSE: James W. Hellwege
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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ZIF: 22202
COMPUTER EDADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR-1994
CLASSIFICATION NUMBER: US/07/872,129
FILING APPLICATION NUMBER: US/07/872,129
FILING APPLICATION NUMBER: US/07/872,129
FILING APPLICATION NUMBER: US/07/872,129
FILING APPLICATION NUMBER: US/07/872,129
FILING COCKET UNMBER: 28,808
REGISTRATION NUMBER: 28,808
REGISTRATION ACCKET NUMBER: 516762
FUNDAME: DAMES SEQUENCE CHARACTERISTICS:
FUNDAME: TENACTERISTICS:
FUNDAME: DAMES ACCTERISTICS:
US-09-180-100-21
US-09-180-100-23
US-09-180-100-23
US-08-6828-683A-22
US-08-050-319B-2
US-08-050-319B-2
US-08-465-982-5
US-08-465-982-4
US-08-465-982-4
US-09-612-033B-6
US-09-612-033B-6
US-09-612-033B-6
US-09-612-033B-6
US-09-623-323-57
US-08-828-60
US-08-828-828-80
US-08-828-838-87
US-08-828-838-87
US-08-828-838-87
US-08-828-838-87
US-08-828-838-87
US-08-828-838-87
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Patent No. 5874546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 153 amino acida
TYPE: amino acid
TOPOLOGY: linear
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76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 117
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         118 EKQNTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,862
FILING DATE: 07-JUN-1995
CLASSIFICATION TYPER: 11.107267
FILING DATE: 12-OCT-1993
PRIOR APPLICATION NUMBER: IL 194039
FILING DATE: 06-APR-1990
PRIOR APPLICATION NUMBER: IL 91229
FILING DATE: 06-APR-1990
PRIOR APPLICATION NUMBER: IL 9129
FILING DATE: 06-APR-1990
PRIOR APPLICATION NUMBER: IL 9129
FILING DATE: 06-ANG-1989
PRIOR APPLICATION NUMBER: IL 9139
FILING DATE: 18-AMY-1989
ATPONENTY ARRAYION:
AMPRICATION NUMBER: IL 90339
FILING DATE: 18-MAY-1989
ATPONENTY ARRAYION:
AMANE: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 200.5; DB 3; Pred. No. 7.7e-11; 20; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                   APPLICANT: BIGDA, Jacek
APPLICANT: BELETSKY, Igor
APPLICANT: METT, Igor
APPLICANT: ENGELMANN, Hartmut
ITLLE OF INVENTION: TNF INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   3: BROWDY AND NEIMARK
419 Seventh Street, N.W.
                                                                                                               Sequence 3, Application US/08476862
Patent No. 6262239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25,618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 25, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 153 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 29.8
Matches 48; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
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STRANDEDNESS: sin
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                                                                                        US-08-476-862-3
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STATE:
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                              68 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC-----FNCSLCLN-GTVH----LSCQ 117
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76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
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                                                                                          133 RRDIDCGICLPGFYEHGDGCVSCPISTLGSCPE--RCAAVC 171
                                                                                                                           133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 200.5; DB 3;
Pred. No. 7.7e-11;
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                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: WALLACH, David
APPLICANT: WALLACH, David
APPLICANT: BELETSKY, IGOR
APPLICANT: BELETSKY, IGOR
APPLICANT: BELETSKY, IGOR
APPLICANT: BELETSKY, IGOR
TITLE OF INVENTION: TNF LIGANDS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/115,685
FILING DATE:
                                                                                                                                                                                                                                                 Sequence 12, Application US/08477347
Patent No. 6232446
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APPLICATION NUMBER: 1L 106271
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-1197
TELEFAX: 202-737-3528
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INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 153 amino acids TYPE: amino acid STRANDEDNESS: single
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MEDIUM TYPE: PLOPBY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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29.8%;
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Best Local Similarity
Matches 48; Conserva
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TELEX: 2'
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Gaps

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76 SQVALENCSAVADTRCGCKPGWFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 153;
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29.8%; Pred. No. 7.7e-11;
tive 20; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 RRDIDCGICLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 EKQNTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 153
                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/800,909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: BROWDY, ROGER L. RECISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH=12A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METT, IGOr
TITLE OF INVENTION: TNF LIGANDS
    TNF INHIBITORS
                                                                     ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: IL 94039
FILING DATE: 06-ARR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 18-MAY-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/09800908
Patent No. 6602931
GENERAL INFORMATION:
APPLICANT: WALLACH, David
                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIGDA, Jacek
BELETSKY, Igor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                            COMPUTER READABLE FORM:
NUMBER OF INVENTION: TW
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                 CITY: Washingt
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                    20004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCOACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.3%; Score 200.5; DB 3; Length 153;
29.8%; Pred. No. 7.7e-11;
tive 20; Mismatches 72; Indels 21; Gaps
                                                                                                                                                                                                     APPLICANT: TTOH, Nacto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 11
CORRESPENDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
STREET: P.O. BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                    STAIL:
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
GOERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/468,560C
FILING DATE: 06-UUN-1995
FILING DATE: 06-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 EKONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 153
    118 EKQNTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 153
                                                                                                         Sequence 4, Application US/08468560C
Patent No. 6270998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WIRPHY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 702.205.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09800909
Patent No. 6555111
GENERAL INFORMATION:
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BELETSKY, Igor
METT, Igor
ENGELMANN, Hartmut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 153 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 29.8*
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein US-08-468-560C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Gaps

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76 SQVALENCSAVADTRCGCKPGWFVEC --- QVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 53, Application US/09523323
; Sequence 53, Application US/09523323
; Patent No. 6635743
; GENERAL INFORMATION:
; APPLICANT: EDNEY, Reinhard
; APPLICANT: EDNEY, Stephen
; APPLICANT: Ulrich, Stephen
; APPLICANT: Ulrich, Stephen
; APPLICANT: ApplicATION Stephen
; APPLICANT: L48.065000C
; CURRENT APPLICATION NUMBER: US/09/523,323
; CURRENT APPLICATION NUMBER: 06/168,380
EARLIER PILING DATE: 1999-12-02
; EARLIER PLING DATE: 1999-08-11
; EARLIER PLING DATE: 1999-08-11
; EARLIER PLING DATE: 1999-08-11
; EARLIER PLING DATE: 1999-03-16
; EARLIER PLING DATE: 1999-03-11
; EARLIER PLING DATE: 1999-02-19
; EARLIER PLING DATE: 1999-02-19
; EARLIER PLING DATE: 1999-02-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 EKQNTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 153
  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.3%; Score 200.5; DB 4; 29.8%; Pred. No. 7.7e-11; iive 20; Mismatches 72;
                                                                                                                                                                                                                                                               FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: MARSCHARG, Diane L.
REFERENCE/DOCKET NUMBER: 35,600
TELECOMMUNICATION INFORMATION:
                                                                                                                                  APPLICATION NUMBER: US/08/828,683A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                           FILING DATE: 31-Mar-1997
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/625328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 154 amino acide TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        650/225-5416
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NMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 29.81
Matches 48; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR
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                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/800,908
FILING DATE: 08-Mar-2001
CLASSIFICATION: <UNKnOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/08828683A
Sequence 12, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: WALLACH=10
                   CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIWARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-800-908-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/477,347
FILING DATE: «UNKNOWN»
APPLICATION NUMBER: 1L 106271
FILING DATE: 08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: South San Francisco
                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ 1D NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: gingle
NUMBER OF SECUENCES: 17
                                                                                                                                                                                 ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-828-683A-12
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76 SOVALENCSAVADTRCGCKPGWFVEC --- OVSQCVSSSPFYCQPCLDCGALHRHTRLLCS 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCOACDEOA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 EKONTVCTCHAGFFLRENECVSC----SNCKKSLECTKLC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: 8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,087A FILING DATE: 08-SEP-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.3%; Score 200.5; DB 3; 29.8%; Pred. No. 8.1e-11; tive 20; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-232-087A-10

Sequence 10, Application US/08232087A

Sequence LO. Se66372

GENERAL INFORMATION:
APPLICANT: Stein, Harald
APPLICANT: Latza, Ute
APPLICANT: Latza, Ute
TITLE OF INVENTION: Lymphoid CD30-Antigen
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
CIPDEN::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFRENCE/DOCKET NUMBER: 756-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
                                                                NAME: Zindrick, Thomas K.
REGISTRATION NUMBER: 32,185
REFERENCE/DOCKET NUMBER: A-4
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       not relevant
                      ATTORNEY/AGENT INFORMATION NAME: Zindrick Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 154 amino acids
                                                                                                                                                                                                                                                          : 161 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . protein
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                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-326-394-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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CLASSIFICATION:
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FRAGMENT TYPE:
   FILING DATE:
                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 GQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQC----FNCSLCLN-GTVH----LSCQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLR-HCLSCSKCRKEM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 HKKIGLPCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09326394
Sequence 2, Application US/09326394
Batent No. 6306820
GENERAL INFORMATION:
APPLICANT: Bendele, Alison M.
APPLICANT: Sennello, Regina M.
APPLICANT: Edwards, Carl K.
TITLE OF INVENTION: COMBINATION THERAPY USING A THF BINDING TITLE OF INVENTION: PROTEIN FOR TREATING THF-MEDIATED DISEASES NUMBER OF SEQUENCES:
ADDRESSEE: Amgen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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ZIP: 91320-1789
COMPUTER READBLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/326,394
FILING DATE: 08-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 19.3%; Score 200.5; DB 4; Best Local Similarity 29.8%; Pred. No. 7.7e-11; Matches 48; Conservative 20; Mismatches 72;
                              EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 09/003,886
EARLIER APPLICATION NUMBER: 08/822,953
EARLIER FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: 06/822,953
EARLIER PELING DATE: 1997-03-21
EARLIER APPLICATION NUMBER: 66/013,923
EARLIER PELING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO S
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FILING DATE: 06-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,355
FILING DATE: 23-DAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 07-PEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050
EARLIER APPLICATION NUMBER: 09/027,287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Amgen Inc.
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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; ORGANISM: Homo sapiens
US-09-523-323-53
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                                                                                                                                                                                                                                  9 HPQNNSICCTKCHKGTYLYNDCPGPGQDTDCDECESQSFTASENHLR-HCLSCSKCRKEM 67
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                                                                                                                                                                                                      16 HKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQA
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                                                                                                                                                            Gaps
                                                                                                           Query Match
19.1%; Score 198.5; DB 2; Length 154;
Best Local Similarity 30.4%; Pred. No. 1.2e-10;
Matches 49; Conservative 23; Mismatches 68; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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18.9%; Score 196; DB 3; Length 139;
Best Local Similarity 31.5%; Pred. No. 1.8e-10;
Matches 45; Conservative 17; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                   133 RRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPE--RCAAVC 171
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13. Application US/09855266A
Patent No. 6784284
GENERAL INFORMATION:
APPLICANT: Kimura, Naoki
APPLICANT: Toyoshima, Tomoko
TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE RERENCE: 06501-040002
CURRENT APPLICATION NUMBER: US/09/855,266A
                  LOCATION: 1..154

OTHER INFORMATION: /note= "TNFR1, see Fig. US-08-232-087A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 122, Application US/08706945D
Patent No. 6369027
GENERAL INFORMATION:
APPLICANT: Lacey, Milliam
APPLICANT: Calzone, Frank
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
FILE REFERENCE: A-378CIP
CURRENT APPLICATION NUMBER: US/08/706,945D
CURRENT FILING DATE: 1996-09-03
PRIOR APPLICATION NUMBER: 08/577,788
PRIOR FILING DATE: 1995-12-22
NUMBER OF SEQ ID NOS: 145
SOFFWARE: Patentin version 3.1
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ORGANISM: Homo sapiens
US-08-706-945D-129
NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -08-706-945D-129
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Sequence 4, Application US/09146950A
Patent No. 6287808
GENERAL INFORMATION:
APPLICANT: BUSIGLA, SAMANTHA J.
TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404,057001
CURRENT APPLICATION NUMBER: US/09/146,950A
CURRENT FILING DATE: 1988-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4.
TENGENT 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 QACDEQASQVALENCSAVADTRCGCKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTR 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 KTCRKEMSQVEISPCQADKDTVCGCK----ENQFQRYLSETHFQC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 LLCSRRDTDCGTCLPGFYEHGDGCVSCPTSTLGSCPERCAAVC 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                17.8%; Score 185; DB 4;
28.8%; Pred. No. 1.5e-09;
tive 16; Mismatches 58;
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CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 09/411,722
PRIOR PELING DATE: 1999-10-01
PRIOR PELING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: PCT/JP98/01511
PRIOR APPLICATION NUMBER: JP 9/099653
PRIOR FILING DATE: 1997-04-01
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-146-950-20
Sequence 20, Application US/09146950A
Patent No. 6287808
GENERAL INFORMATION:
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Matches 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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Matches 46; Conserv
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TYPE: PRT
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APPLICANT: Busfield, Samantha J.

TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 09404/057001
CURRENT APPLICATION NUMBER: 18/09/146,950A
CURRENT FILING DATE: 1998-09-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 LRASRNCSRTENAVCGCSPGHF-----CIVQDGDHCAACRAYATSSPGQRVQKGGTES 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Ebner, Reinhard

APPLICANT: Yu, Guo-Liang

APPLICANT: Ruben, Seeven M.

APPLICANT: Ruben, Seeven M.

APPLICANT: Ullrich, Stephen

APPLICANT: Ullrich, Stephen

APPLICANT: Ullrich, Stephen

TITLE OF INVENTION: Apoptorsis Inducing Molecule II and Methods of Use

TITLE PARENCE: 1488.065000C

CURRENT APPLICATION NUMBER: US/09/523,323

CURRENT APPLICATION NUMBER: 60/168,380

EARLIER PILING DATE: 1999-12-02

EARLIER PILING DATE: 1999-00-03-10

EARLIER PILING DATE: 1999-00-04

EARLIER PILING DATE: 1999-06-04

EARLIER PILING DATE: 1999-06-04

EARLIER PILING DATE: 1999-02-19

EARLIER PILING DATE: 1999-02-03

EARLIER PILING DATE: 1999-02-19

EARLIER PILING DATE: 1998-02-0

EARLIER PELING DATE: 1998-02-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.5%; Score 182; DB 3; Length 159; 30.7%; Pred. No. 3.7e-09; vative 14; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 RDTDCGTCLPGFYEHGDGCVSCPTSTLGSC 163
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EARLIER APPLICATION NUMBER: 60/030,157
EARLIER FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 56
LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5-09-523-323-56
Sequence 56, Application US/09523323
Patent No. 6635743
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
US-09-146-950-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46;
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Matches
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THE PLANT WEST

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein June 27, 2005, 14:31:28 ; Search time 38 Seconds (without alignments) 202.562 Million cell updates/sec Run on:

80

US-10-081-280-6_COPY_338_417

1 VMDAVPARRWKEFVRTLGLR......ERMGLDGCVEDLRSRLQRGP Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues

Searched:

26016 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 80 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES æ

	Description	hypothetical prote	conserved hypothet	hypothetical prote	5	hypothetical prote	_	conserved hypothet	hypothetical prote	-4		hypothetical prote	repressor protein	probable damage-in			hypothetical prote	probable phage tai	integrase-related	glutaredoxin - The	host factor for ly	factor for	slyX protein - Esc	hypothetical prote	probable phage tai	keratin 15, type I	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote
SOMMENTES	ΩI	F71080	G69463	E69386	D69499	A84092	H84353	A82881	D83610	C69333	A96702	G83940	JH0129	AH0619	A75099	H70576	F83985	AC1037	H70799	F72303	G91153	C85999	A49988	B75199	AG0927	B55682	F81899	F69871	AE2659	C97441
	80	8	7	~	~	7	~	7	7	~	~	7	~	7	7	~	7	~	Н	~	7	7	~	~	~	~	~	~	~	7
	Length	74	71	72	73	79	78	72	9	61	67	64	68	79	72	16	25	67	71	80	72	72	72	74	67	68	70	62	75	75
* Ouery	Match	R		12.2		12.2	12.0	11.6	11.4	11.4	11.4	11.3	11.3	11.3	11.1	11.1	11.0	10.9	10.9	10.9	10.8	10.8	10.8	10.8	10.7	10.7	•	10.5	•	10.5
	Score	52.5	50.5	50.5	50.5	50.5	49.5	48	47	47	47	46.5	46.5	46.5	46	46	45.5	45	45	45	44.5	44.5	44.5	44.5	44	44	44	43.5	٠	43.5
esult	No.	н	7	ო	4	S	9	7	œ	σ	10	1	12	13	14	12	16	17	18		20						56		28	53

probable ribosomal	Icd-like protein [hypothetical prote	ribosomal protein	hypothetical prote	conserved hypothet	mineralocorticoid	M protein precurso	hypothetical prote	hypothetical prote	M protein precurso	conserved hypothet	hypothetical prote	hypothetical prote	50S ribosomal prot	hypothetical prote
E70644	A90826	H81238	T45384	F64547	F69219	153270	S60803	A82086	F72592	560835	D69283	AD2769	H83960	D81212	C69327
N	~	~	~	~	~	~	~	~	~	~	~	~	~	~	0
65	65	65	71	73	77	47	28	77	79	80	37	61	73	77	36
0.4	10.4	10.4	10.4	10.4	10.4	10.3	10.3	10.3	10.3	10.3	10.2	10.2	10.2	10.2	10.0
7			~	m	m	'n	'n	'n	'n.	'n	7	42	7	7	'n
43 1	43	43	4	4	4	42	42.5	42	42	42	•	Ì	•	•	41.5

ALIGNMENTS

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Pypotherical protein PHS027 - Pyrococcus horikoshii
C;Species: Pyrococcus
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
M; Obfuku, Y.; Fundhashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic an
A;Accession: F71080
A;Accession: F71080
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-74 - KNA
A;Residues: 1-74 - KNA
A;Residues: UNA
A;R
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G69463
conserved hypothetical protein AF1712 - Archaeoglobus fulgidus
c;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: G6943
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R;Klenk, H.P.; Clayton, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; Ketchum, K.A.; Dodson, J.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Wosse, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: G69463
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-71 cKLE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 12.7%; Score 52.5; DB 2; Length 7 Local Similarity 27.3%; Pred. No. 82; Length 7 les 18; Conservative 14; Mismatches 27; Indels
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67 VEGMKE 72
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Best Local S:
Matches 18
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Conserved hypothetical UUS18 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Mug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: A92881 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mini A;Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Vng2035h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Palobacterium sp. NRC-1
C;Accession: H84153
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H., Alam, M.; Freitas, T. 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liż
A;Ritle: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE002150; GB:AF222894; NID:g6899515; PIDN:AAF30931.1; GSPDB:GN001;
A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                   F.; Hiran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9K736; GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB072?
A;Experimental source: strain C-125
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hypothetical protein BH3537 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A84092
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Ree: 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83569; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
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Pred. No. 1.8e+02;
7; Mismatches 23;
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27.8%;
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Best Local Similarity 27.6*
Matches 16; Conservative
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Matches 15; Conservative
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-72 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-79 <STO>
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A;Molecule type: DNA
A;Residues: 1-78 <STO>
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Cispecies: Archaeoglobus fulgidus
Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cipate: 05-Dec-19986
Cipate: 05-Dec-19986
Cipate: 05-Dec-1997
Cipate: 06-July Cipate
Cipate: 06-July 
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R; Klenk, H.D.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson : Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C. A; Tille: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A; Reference number: A69250; MUID:98049343; PMID:9389475

A; Status; preliminary; nucleic acid sequence not shown; translation not shown
A,Cross-references: UNIPROT:028561, GB:AE000985; GB:AE000782; NID:g2689308; PIDN:AAB8953
C;Superfamily: Methanococcus jannaschii hypothetical protein MJ0975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:029171; GB:AE001028; GB:AE000782; NID:92689351; PIDN:AAB9016
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C;Superfamily: uncharacterized conserved protein
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec_1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                      Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                          4 IIEAVYQKGVLKPLRKVSLREGEIVKVEIRETKKVTGRFYAKLRELEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 73;
                                                                                                                                                                                                                                                                                                                                                                        1 VMDAVPARRWKEFVRTLGLREAEIEAVEVE----IGRFRDQQYEMLKR
                                                                                                                                                                                                                                                                          18; Indels
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                                                                                                                                                           Query Match
12.2%; Score 50.5; DB 2;
Best Local Similarity 32.7%; Pred. No. 1.3e+02;
Matches 16; Conservative 10; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 12.2%; Score 50.5; DB 2; Best Local Similarity 27.7%; Pred. No. 1.3e+02; Matches 13; Conservative 8; Mismatches 19;
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Best Local Similarity 27.8*
Matches 15; Conservative
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A; Residues: 1-73 < KLE>
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DB 2;

11.6%; Score 48; DB 28.0%; Pred. No. 2.4e iive 10; Mismatches

Query Match Best Local Similarity 28.0* Matches 7; Conservative

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A;Gene: UU518 A;Genetic code: SGC3

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EYIKTLGRNONAVVYIQTKDGKFQD 65 12 EFVRTLGLREAEIEAVEVEIGRFRD 36

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C;Species: Arabidopsis thallana (mouse-ear cress)
C;Bate: 02-Mar-2001 #sequence_revision - Arabidopsis thallana (mouse-ear cress)
C;Bate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A96702
R;Theologis, A:; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
CA.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Aththors: Maroney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Hitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reterence number: A86141; MUID:21016719; PMID:11130712
A;Retus; preliminary
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C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G89340
R;Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and ¢ A;Reference number: A33550; MUID:20512582; PMID:11058132
A;Accession: G89340
A;Status: preliminary
A;Reference DNA
A;Residues: 1-64 <STO>
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A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2327
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N;Alternate names: repressor protein F
C;Species: Bacherichia coli
Species: Bacherichia coli
C;Species: Bacherichia coli
C;Date: plasmid RSF1010 is a broad-host-range plasmid belonging to incompatibility group
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: JH0129; PS0292
R;Sch01z, P.; Haring, V.; Wittmann-Liebold, B.; Ashman, K.; Bagdasarian, M.; Scherzinger, A;C, 271-288, 1989
A;Title: Complete nucleotide sequence and gene organization of the broad-host-range plasm
A;Reference number: JH0123; MUID:89232758; PMID:2653965
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A;Residues: 1-67 <STO>
A;Cross-references: UNIPROT:Q9C9V8; GB:AE005173; NID:g6553903; PIDN:AAF16569.1; GSPDB:GN(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 KEF--VRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 2; Length 67;
Pred. No. 2.9e+02;
5; Mismatches 13; Indels
unknown protein, 70659-70456 [imported] - Arabidopsis thaliana
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34.8%;
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Matches 16; Conservative
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Cibate: 15-Sep-2000 #sequence_revision 15-55, warrener, P.; Hickey, M.J.; Br Riscover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br Riscover, C.K.; Pham, X.O.; Erwin, A.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyaccesion: C6933
Rivienk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodson Frklenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodson. Fleischmann, R.D.; Quackenbush, J.; Gcayne, J.D.; Weidman, J.F.; McDonald, L. Godylek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woses, C.R.; Venter, J.C. A; Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaech A; Reference number: A69250; MUID:98049343; PMID:9389475
A; Reference number: A69250; MUID:98049343; PMID:9389475
A; Recession: C69333
A; Molecule type: DNA
A; Residues: 1-61 < KLE>
A; Residues: 1-61 < KLE>
A; Residues: 1-61 < KLE>
A; Cross-references: UNIPROT:029590; GB:AE001058; GB:AE00782; NID:92689381; PIDN:AAB9057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-60 <STO>
A;Cross-references: UNIPROT:Q916K6; GB:AE004466; GB:AE004091; NID:g9946120; PIDN:AAG0367
A;Experimental source: strain PAO1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein PA0284 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein AF0667 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Pseudomonas aeruginosa
Bate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
                 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 2; Length 60;
Pred. No. 2.6e+02;
6; Mismatches 15; Indels
Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.4%; Score 47; DB 2; Length 61; 34.5%; Pred. No. 2.6e+02;
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19 LREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPA

ઠે g

ch 11.4%; 1 Similarity 36.4%; 12; Conservative

Best Local Similarity Matches 12: Conserv

Query Match

A; Gene: PA0284

7; Mismatches

10; Conservative

Best Local Similarity Matches 10; Conserv

Query Match

35 RDQQYEMLKRWRQQQPAGLGAVYAALERM 63

ઠે 셤 RESULT 10 A96702

A; Accession: JH0129

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Search completed: June 27, 2005, 14:41:37 Job time : 40 secs
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nes 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: Rv2132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C, Genetics:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable damage-inducible protein STY1032 [imported] - Salmonella enterica subsp. enterically cispecies: Salmonella enterica subsp. enterica serovar Typhi
A,Note: this species has also been called Salmonella typhi
C;Bate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AH0619
R;Parkhill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H. T; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovals A;Accession: AH0619
                                                A;Cross-references: UNIPROT:Q52350; GB:M28829; NID:g152577; PIDN:AAA26449.1; PID:g152585
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A;Reference number: A75001
A;Accession: A75099
                                                                                                   A;Molecule type: protein
A;Residues: 1-18 <SCH2>
C;Comment: This protein binds to the operator region of a promoter located at upstream
                                                                                                                                                                                                                                                                                                                                            7
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                                                                                                                                                                                                                                                                                                                                                                                       3 DAVPARRWKEFVRTLGLREAEIEAVBVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALER 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 RTLGLREAEIEAVEVEIGRFRDQQYE----MLKRWRQQQPAGLGAVYAALERMGLDGCVE 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 RTKQLPEGAVPALEKELITRLONGYENCNLTIRRGSOD---GLSIVGAA-----DGDKK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein PAB3293 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46.5; DB 2; Length 79;
Pred. No. 3.9e+02;
8; Mismatches 24; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                            31; Gaps
                                                                                                                                                                                                                                                                                Query Match
11.3%; Score 46.5; DB 2; Length 68;
Best Local Similarity 20.8%; Pred. No. 3.3e+02;
Matches 15; Conservative 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          C,Accession: A75099
R,anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.3%;
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Best Local Similarity 32.8
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 MGLDGCVEDLRS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----CLEELRA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 DLRSRLQ 77
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A; Molecule type: DNA
A; Residues: 1-68 <SCH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-79 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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                                                                        A, Accession: PS0292
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                                                                                                                                                                                                       A;Gene: cac
A;Genome: plasmid
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                                                                                                                                                                               C, Genetics:
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Pypothetical protein Rv2132 - Mycobacterium tuberculosis (strain H37RV)

CjSpecies: Mycobacterium tuberculosis

CjSpecies: Mycobacterium tuberculosis

CjAccession: H70576

RjCole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Ritle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome FA;Reference number: A70500; MUID:9829597; PMID:9634230
A;Cross-references: UNIPROT:09UZG5; GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB50094
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB3293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:006243; GB:Z95388; GB:AL123456; NID:g3261759; PIDN:CAB08638.1
A;Experimental source: strain H37Rv
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-76 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 RSIGLSEAVNELIRAGLTKRQVANRFQQQTYDM------GEGIDYSNIGDAIET-- 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 RTLGLREAEIEAVEVEI-----GRFRDQQYEMLKRWRQQQPAGLGAVYA----ALERMG
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                     Length 72
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                              11.1%; Score 46; DB 2;
38.7%; Pred. No. 4e+02;
ive 8; Mismatches
                                                                                                                                                                                                                                                                                                                      14 VRTLGLREAEIEAVEV--EIGRFRDQQYEML 42
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 38.73
Matches 12; Conservative
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Q8wtg4 oreophoetes Q8wti4 aretaon asp Q8wtf1 timema knul Q8wtg2 phyllium bi

giardia lam staphylococ

staphylococ ctenomorpho heteroptery

OGDXY6 OGDXY6 OGDXY7 OGWTH4 OBWTH8

arabidopsis

09ppx1 06q6g0 024410

Н

OM protein

Run on:

Sequence:

Minimum DB Maximum DB

Database

Result

Searched:

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R HSSP; O9EZJ8; IKU3.

R GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.

GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.

GO; GO:0005700; F:transcription factor activity; IEA.

GO; GO:0005740; F:transferase activity; IEA.

GO; GO:000535; F:rensferase activity; IEA.

GO; GO:000535; F:transcription of transcription, DNA-dependent; IEA.

R D; GO:000535; F:transcription initiation; IEA.

R InterPro; IPR007630; Sigma 70 r4.

R InterPro; IPR007631; Sigma 70 r4.

R RINTS; RR0046; SIGMA 70 r4.

R RNNTS; RR0046; SIGMA 70 r4; I.

R ROSITE; PS00716; SIGMA 70 -2; 1.

R Transcription regulation; Transferase; Sigma factor; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 VRTLGLREAE---IEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.3%; Score 59; DB 2; Length 79; ilarity 40.0%; Pred. No. 1.2e+02; Conservative 5; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 AA; 9136 MW; AE74B2F1226CC213 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Q6TG30.
05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                         79
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA polymerase sigma factor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                            Created)
              Q9PPX1
Q6Q6G0
Q24410
Q6DNN4
Q7R0H4
Q6PXY7
Q6PXY7
Q8WTH4
Q8WTH4
Q8WTG4
Q8WTG4
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22; Conserv
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 NCBI_TaxID=303;
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093R97,
01-DEC-2001 (
Name=rpoS;
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Best Local S
Matches 22
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EMBL; 1
HSSP; (
GO; GO;
GO; GO;
GO; GO
GO; GO;
GO; GO
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Q6TG30
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Q7p21 fusobacteri
Q92x19 bacteriopha
Q6czu0 erwinia car
Q8Ly5 methanopyru
Q72gh9 thermus the
Q8u39 pyrococcus
Q719x2 synechococc
Q914F5 oryza sativ
G6pxy4 staphylococ
Q918 staphylococ
Q918 staphylococ
Q918 arthrobacte
Q8au5 spendomonas
Q7eyn4 oryza sativ
Q7v7d7 prochloroco
Q28.61 archaeoglob
Q29.71 archaeoglob
Q29.71 archaeoglob
Q29.73 bacillus ha
Q8d62 vibrio vuln
Q8rxy shewanella
Q8cxv shewanella
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Q883a4 pseudomonas
Q716n0 mycobacteri
                                                                                                                                        (without alignments)
243.847 Million cell updates/sec
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Compugen Ltd.
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                GenCore version (c) 1993 - 2005
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Q8H4R5
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Q6PXY4
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Q72GH9
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Q8ECW2
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Q7MKX6
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Q6TG30
Q7P3Z1
Q9ZXL9
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Q9HINM4
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

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Best Local Similarity
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                                                                                                                                                                   Bacteriophage phi
                                                                                                                                                                                                                   NCBI_TaxID=35343;
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25-OCT-2004
25-OCT-2004
                                                                                                   01-MAY-1999
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01-MAR-2004
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Q6CZU0
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                                                                                                                                                         Scott A., Meakins D., Page W.J.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: Signam factors are initiation factors that promote the attachment of RNA polymerses to specific initiation sites and are then released (By similarity).

- Initiation sites and are then released (By similarity).

- SIMILARITY: Bealongs to the sigma-70 factor family.

EMBL; AY422193; AA590415.1; --.

GO; GO:0016987; F:sigma factor activity; IEA.

GO; GO:0006352; F:transcription factor activity; IEA.

GO; GO:0006352; P:regulation of transcription, DNA-dependent; IEA.

GO; GO:0006352; P:regulation initiation; IEA.

InterPro; IPR00043; Sigma70 r4.

Refam; PP04545; Sigma70 r4.

RENINTS; PR00046; SIGMA70FCT.

RENINTS; PR00046; SIGMA70FCT.

RENINTS; PR0016; SIGMA70FCT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 VRTLGLREAE---IEAVEVEIG----RFRDQQYEMLKRWRQQQPAGLGAVYAALERMGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 49256;
Karpatral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A., Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T., Gardner W. L., Werbeek R., Kyrpides N.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                               Azomonas macrocytogenes.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 54.5; DB 2; Length 59; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusobacterium nucleatum subsp. vincentii ATCC 49256.
Bacteria, Fusobacteria, Fusobacterales; Fusobacteriaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Indels
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1, AABF01000154; EAA23321.1; -.
JENCE 59 AA; 6808 MW; 615C5DF19B318E86 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.8%; Score 57; DB 2; I
39.0%; Pred. No. 1.3e+02;
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                 Stationary phase sigma factor (Fragment)
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ilarity 37.2%;
Conservative
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Best Local Similarity 39.0
Matches 23; Conservative
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nes 16; Conserv
                                                                                                                                                 STRAIN=ATCC 12334;
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                                                                                               NCBI_TaxID=69962;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
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STRAIN=SCR1 1043 / ATCC BAA-672;
STRAIN=SCR2 1043 / ATCC BAA-672;
Bell K.S., Sebainia M., Pritchard L., Holden M.T.G., Hyman L.J.,
Bell K.S., Sebainia M., Pittchard L., Holden M.T.G., Hyman L.J.,
Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
Atkin R., Bason N., Bencley S.D., Churcher L.J.C., Mungall K.,
Praser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.,
"Genome sequence of the enterobacterial phytopathogen Erwinia
carotovora subsp. atroseptica and characterization of virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Makayama K., Kanaya S., Ohnishi M., Terawaki Y., Hayashi T.;
"The complete nucleootide sequence of phiCTX, a cytotoxin-converting phage of Peudomonas aeruginosa: implications for phage evoltion and horizontal gene taransfer via bacteriophage.";
Mol. Microbiol. 31:399-419(1999).
BMBL; AB008550; BAA36234.1;
InterPro; IPR00861; Tail. Y.
Pfam; PF05489; Phage tail. X; 1.
SEQUENCE 69 AA; 7436 MW; D2E35A698F195CC0 CRC64;
                                                                                                                                                                                 Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
P2-like viruses.
                                                                          01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Pseudomonas aeruginosa phage phi CTX, complete genome sequence.
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Pred. No. 3.5e+02;
4; Mismatches 9; Indels
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EMBL; BX950851; CAG76958.1; -.
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  69 AA.
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                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=phiCTX-c;
MEDLINE=99157549; PubMed=10027959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacteriaceae; Pectobacterium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Microbiol. 3:861-868(1989)
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PRELIMINARY;
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61 ERMGLDGCVE
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  NCBI_TaxID=262724;
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                                                                    PubMed=15064768;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8U397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanopyrus kandleri.
Archaea; Buryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                            Gaps
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STRAIN=AV19 / DSM 6324 / JCM 9639;

STRAIN=AV19 / DSM 6324 / JCM 9639;

MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;

MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;

Slegarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,

Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,

Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,

Malykh A.G., Koohin E.V., Kozyavkin S.A.;

"The complete genome of hyperthermophile Methanopyrus kandleri AV19

and monophyly of archaeal methanogens.";

Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
OrderediocusNames=TTC1869;
Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
Bacteria; Deinococcus-Thermus; Deinococcus Thermales; Thermaceae; Thermace.
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                                                                                                                                                                                                                                                                                                       1 MIIPWQQLDPETLDSIIESFVLREGTDYGEQER-SLAQKVEDIRSQLQSG 49
                                                                                                                                                                                                                                                          41 MLKRWRQQQPAGL-----GAVYAALERMGLDGCVEDLRSRLQRG
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                                                                                                                                                               Length 78;
                                                                                                                                                                                                            16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003 (TrEMBLrel. 21, Last sequence update)
Predicted RNA-binding protein containing the S4 domain.
Methanopynie bashares WK0398;
                                                                                        Complete proteome, Hypothetical protein.
SEQUENCE 78 AA; 8894 MW; CC29D8DC6F12BF9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 AA; 8930 MW; 87B143AA16BAF785 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                             13.1%; Score 54; DB 2; llarity 36.0%; Pred. No. 4e+02; Conservative 4; Mismatches 1.
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EMBL; AE010336; AAM01613.1; -.
GO; GO:0003723; F:RNA binding; IEA.
                      InterPro; IPR010648; UPF0270.
Pfam; PF06794; UPF0270; 1.
PIRSF; PIRSF006169; UCP006169; 1.
InterPro; IPR008227; UCP006169.
InterPro; IPR010648; UPF0270.
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PROSITE; PS50889; S4; 1.
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Matches 22; Conserv
                                                                                                                                                                                 Local Similarity
hes 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
Henne A., Brueggemann H., Raasch C., Wiezer A., Hartsch T., Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R., Jacobi C., Starkuviene V., Schlenczeck S., Dencker S., Huber R., Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.; "The genome sequence of the extreme thermophile Thermus thermophilus.";
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Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE010180; AAL80697.1; --
Pfam; PF04014; SpoyT AbrB; 1.
TIGRFAMS; TIGR01439; lp_hng_hel_AbrB; 1.
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                                                                                                                                                                                                                                                                                                                                         12.8%; Score 53; DB 2; Length 62; 29.3%; Pred. No. 4e+02; tive 14; Mismatches 25; Indels
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Synechococcus sp. (strain WH8102).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
                                                                                                                                                                                            Nat. Biotechnol. 22:547-553(2004).
EMBL, AE017307; AAS8211.1; Complete protecome; Hypotherical protein.
SEQUENCE 62 AA; 7921 MW; 0D272F18D427D6EA CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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12.0%; John Vol. 4e+0
Best Local Similarity 29.3%; Pred. No. 4e+0
Matches 17; Conservative 14; Mismatches
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2003 (TrEMBLrel. 24,
Hypothetical protein PF0573.
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InterPro; 1PR006339; AbrB trans reg.
InterPro; 1PR007159; SpovT_AbrB.
Pfam; PF04014; SpovT_AbrB, 1
TIGRFAMS; TIGR01439; 1p_hng_hel_AbrB; 1.
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InterPro; IPR000850; GroEL-ATPase.
Pfam; PP00118; Cpn60_TCP1; 1.
ATP-binding; Chaperone.
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05-JUL-2004 (TrEMBLrel, 27, 05-JUL-2004 (TrEMBLrel, 27, 05-JUL-2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 27.39
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Best Local Similarity 31.2
Matches 15; Conservative
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 Pyrococcus horikoshii.
                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. SEQUENCE 74 AA;
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                                                                                      SEQUENCE FROM N.A.
                                                    NCBI_TaxID=53953;
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SEQUENCE
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                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=0J1457_D07.108; Synonyms=0J1058_B11.129;
Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                            MEDLINE-2285697; PubMed=12917641; DOI=10.1038/nature01943; Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L., Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarren J., Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.; "The genome of a motile marine Synechococcus."; "The genome of a motile marine Synechococcus."; Mature 424:1037-1042(2003).

EMBL; BX569689; CABO6645.1; -- Complete proteome; Hypothetical protein.

SEQUENCE 78 AA; 8562 MW; 8CCEC4D8C72C7321 CRC64;
                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki T., Matsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 12.7%; Score 52.5; DB 2; Length 70; Local Similarity 31.7%; Pred. No. 5.2e+02; Nes 19; Conservative 8; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
52-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein OJ1457_D07.108 (Hypothetical protein OJ1058_B11.129).
                                                                                                                                                                                                                           Length 78;
                                                                                                                                                                                                                         / Match 12.8%; Score 53; DB 2; Length 78; Local Similarity 34.1%; Pred. No. 5.1e+02; Ne 14; Conservative 14; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JŪL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003956; BAC21370.1; -.
EMBL; AP003864; BAD30405.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone:0J1457 D07.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                              36 DQQYEMLKRWRQQQPAGLGAVY-AALERM-GLDGCVEDLRS 74
                                                                                                                                                                                                                                                                                                                Gramene, Q8H4R5; -.
Hypothetical protein.
SEQUENCE 70 AA; 7543 MW; 43E9E837A80B9238 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PHS027.
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                                  SEQUENCE FROM N.A.
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NCBI_TaxID=84588;
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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sakine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohtuku Y.,
Punahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
EMBI. AP000004; BAA3004.1; -.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.7%; Score 52.5; DB 2; Length 77; 31.2%; Pred. No. 5.7e+02; tive 11; Mismatches 19; Indels
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Last annotation update)
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Staphylococcus xylosus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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SEQUENCE FROM N.A.
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01-JUN-2003
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MEDLINE=21405725; PubMed=11514508;

MEDLINE=21405725; PubMed=11514508;

DOI=10.1128/19183.18.5262-567.2001;

Baitsch D., Sandu C., Brandsch R., Igloi G.L.;

"Gene cluster on pA01 of Arthrobacter nicotinovorans involved in degradation of the plant alkaloid nicotine: cloning, purification, and characterization of 2.6-dihydroxypyridine 3-hydroxylase.";

J. Bacteriol. 183:5262-5267(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Menendez C., Otto A., Igloi G., Nick P., Brandsch R., Schubach B.,
Bottcher B., Brandsch R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molybdate-uptake genes and molybdopterin-biosynthesis genes on a bacterial plasmid, Characterization of MoeA as a filament-forming protein with adenosinetriphosphatase activity."; Eur. J. Biochem. 250:124-531(1997).
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MEDLINE=99096870; PubMed=9878333; DOI=10.1006/jmbi.1998.2227;
  64
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                                                                                                                                                                                                                                                                                                      Plasmid pA01, and Plasmid pA01.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Micrococcaceae; Arthrobacter.
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MEDLINE=95115562; PubMed=7815950;
Grether-Beck S., Igloi G.L., Pust S., Schiltz E., Decker K.,
                         LGLREAEI BAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMG
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Last annotation update)
                                                                                                                                                    70 AA
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MEDLINE=96172783; PubMed=8588735;
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C-2004 (TrEMBLrel. 27, 1
(Hypothetical protein)
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                                              DOI=10.1128/JB.185.6.1976-1986.2003;
Igloi G.L., Brandsch R.;
"Sequence of the 165-kilobase catabolic plasmid pAO1 from Arthrobacter
"Sequence of the 165-kilobase catabolic plasmid pAO1 from Arthrobacter
nicotinovorans and identification of a pAO1-dependent nicotine uptake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Buell C.R., Joardar V., Lindeberg M., Salengut J., Paulsen I.T., Madupu R., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Dudsherty S.C., Barinkac L.M., Beanan M.J., Haft D.H., Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q., Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J., Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L., White O., Fraser C.M., Collmer A.; Schneider D.J., Tang X., The complete genome sequence of the Arabidopsis and tomato pathogen Pseudomonas syringae pv. tomatco D63000.;
Peroc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
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Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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Pred. No. 7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                  23; Indels
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                                                                                                                                                                                                                  EMBL, AF373840; AAK64270.1; -.
EMBL, AJ507836; CAD47929.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 70 AA; 7833 MW; 1501DDE147F444FF CRC64;
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66 AA; 7274 MW; 6DD44F84FA4A630C CRC64;
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Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                           Score 52; DB 2; Pred. No. 5.8e+02;
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PLASMID=pAO1;
MEDLINE=22505657; PubMed=12618462;
                                                                                                                                                                system.";
J. Bacteriol. 185:1976-1986(2003)
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Hypothetical protein OSJNBb0011E04.106.

Name-CSJNBb0011E04.106.

Norac Sativa (japonica cultivar-group).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; C Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Enrhartoidaea; Oryzae; Oryza.

NCBI TaxID-39947;

NGI TaxID-39947;

Sasaki T., Matsumoto T., Katayose Y.;

Sasaki T., Matsumoto T., Katayose Y.;

Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AP005443; BAD05624.1; -.

Hypothetical protein.

SEQUENCE 63 AA; 7063 MW; 348C125AE42F427D CRC64;
                                                                                                                                                                                                                                                                                            Query Match
12.2%; Score 50.5; DB 2; Length 63;
Best Local Similarity 32.8%; Pred. No. 7.6e+02;
Matches 21; Conservative 8; Mismatches 20; Indels 15; Gaps
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Search completed: June 27, 2005, 14:40:56 Job time : 174 secs

59 ALER 62 |: | 60 AVRR 63

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Disclosure; Page 37; 58pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG31492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                      ABG31492
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Apo
Apo-3/DR3
Human Apo
Human DR3
Human DR3
Human Apo
Death dom
TWFR1 dom
TWFR1 dom
Human TWF
Human TWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human p55
NOV1 doma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Apo
Human DR5
Human CAR
Tumour ne
Human imm
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Human DR4
Death dom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Death dom
Human DR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Partial h
Chlamydia
                                                                                          June 27, 2005, 14:22:33 ; Search time 158 Seconds (without alignments) 195.828 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                          80
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                                                                                                                                                                                         1 VMDAVPARRWKEFVRTLGLR......ERMGLDGCVEDLRSRLQRGP
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Aac08695 F
Aab26989 F
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Aam89832 B
Adg98743 B
Ado40452 B
Ada49713 B
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Aab99285 H
Aae24868 (
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Ada49709 1
Adg98745 Ado40454 1
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Ado40453
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                                                                                                                                                                                                                                                                                                       1092469
5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                       2105692 segs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                           US-10-081-280-6_COPY_338_417
                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW93613
AAY67948
AAM89832
ADG98743
ADG40452
ADA49713
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AAE24868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADG98744
ADG40453
ADG40453
AABZ6510
AABZ651193
ADG49709
ADG49709
ADG4051
AAM93612
AAM93612
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AAM93612
AAM93612
AAM93699
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geneseqp2003bs:*
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: geneseqp1980s:*
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geneseqp2001s:*
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq length: 0 seq length: 80
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16.2
15.6
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68
67
64.5
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Perfect score:
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                                                            OM protein
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Maximum DB
                                                                                                                                                                                          Sequence:
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Aae38911 Chlamydia		6 Human	Aaw93611 Human Fas	Aab26988 Human CD9	Aam80357 Human hae	Abg31494 Human Apo	Ada49710 Death dom	Adg98746 Fas/Apol	Ado40455 Human Fas	Aae24866 Chlamydia	Aae38909 Chlamydia	Aae24857 Mouse NGF	Aae38900 Mouse NID	Adn46273 Thermococ	Aae24856 Chlamydia	Aae38899 Chlamydia	Aau63529 Propionib	Abm60048 Propionib
4.6		. 4.	4	æ	4	•	æ	æ	•	•	•	•	•	•	•	æ	•	4
AAE38911	AD.TOSBSB	AAW00206	AAW93611	AAB26988	AAM80357	ABG31494	ADA49710	ADG98746	AD040455	AAE24866	AAE38909	AAE24857	AAE38900	ADN46273	AAE24856	AAE38899	AAU63529	ABM60048
S C	ν α	0	~	m	4	ß	9	7	80	Ŋ	Ŋ	Ŋ	ß	œ	ß	'n	4	9
65	, ,	63	68	68	68	77	77	77	77	9	65	71	71	73	9	9	9	9
15.6	14.U		13.9	13.9	13.9	13.9	13.9	13.9	13.9	13.8	13.8	13.8	13.8	13.7	13.6	13.6	13.3	13.3
64.5		57.5	57.5	57.5	57.5	57.5	57.5	57.5	57.5	57	57	57	57	56.5	26	26	52	52

ALIGNMENTS

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Human, Apo-2DCR, Apo-2 ligand, programmed cell death, apoptosis,
neurodegenerative disease; autoimmune, inflammatory.
                                                                                                                                                                                                                  Human Apo-2DcR associated protein #2
ABG31492 standard; protein; 74 AA
                                                                                                                                            (first entry)
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97US-0049911P. 98US-00096500.

Chuntharapai A,

Kim KJ;

Gurney A,

Novel isolated Apo-2DcR polypeptide useful for modulating apoptosis in

The present invention relates to the isolation of novel human polypeptides, designated Apo-2DCR, and the polynucleotide sequences encoding them. Apo-2DCR is capable of binding Apo-2 ligand and is useful for modulating programmed cell death or apoptosis in mammalian cells. Apo-2DCR can be used to produce apo-2DCR antibodies which are useful therapeutically, and can cross-react with other receptors for Apo-2 ligand to block excessive apoptosis in neurodegenerative diseases, or to block potentially autoimmune or inflammatory effects. Apo-2DCR antibodies are also useful in immunchistochemistry staining assays or diagnostic assays for Apo-2DCR, e.g. detecting it's expression in specific cells, tissues or serum, and for the affinity purification of Apo-2DCR from recombinant cell culture or natural sources. The present sequence

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74

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1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAAL 60
                        61 ERMGLDGCVEDLRS
                                     ERMGLDGCVEDLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                           JS2004009552-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 74 AA;
                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                             15-JUL-2004
                                                                                                                                                                                                                                                                 15-JAN-2004.
                                                                                                                        ADO40453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                         ADO40453
                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides novel Apo-2 protein and the nucleic acid encoding the protein. The invention is useful in inducing apoptosis in mammalian cancer cells. The invention is also useful in diagnostic procedures for tissue-specific typing and in generating transgenic animals that are useful in development and screening of reagents. The invention is also useful in development the present sequence is Apo3/DR3 death domain protein.
                                                                                                                                                                                                                                                                                                                    Apo-2; apoptosis; diagnosis; tissue-specific typing; transgenic animal;
                                                                                                                            1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAAL
  to the present
the Seq listing but
                                                                                                            VMDAVPARRWKEFVRTLGLREABIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAAL
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Apo-2 polypeptide or its extracellular or death domain sequence, useful for modulating apoptosis in mammalian cancer cells or for generating transgenic or knockout animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                               92.3%; Score 381; DB 5; Length 74; 100.0%; Pred. No. Se-41; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.3%; Score 381; DB 7; Length 74; 100.0%; Pred. No. 5e-41; ive 0; Mismatches 0; Indels
represents a protein of unknown function relating invention. Note: The present sequence is given in not mentioned elsewhere in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chuntharapai A,
                                                                                                                                                                                                                              ADG98744 standard; protein; 74 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2B; 64pp; English
                                                                                                                                                                                                                                                                                              Apo-3/DR3 death domain protein
                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAY-1997; 97US-0046615P.
09-FEB-1998; 98US-0074119P.
14-MAY-1998; 98US-00079029.
02-NOV-2001; 2001US-00052798.
                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2002; 2002US-00288917.
                                                                                                                                                      ERMGLDGCVEDLRS 74
                                                                                                                                                                  Query Match
Best Local Similarity luv...
As 74; Conservative
                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100...
74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams CW, Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                 cancer; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-897574/82.
                                                                                                                                                                                                                                                                                                                                                                         US2003148455-A1.
                                            Sequence 74 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 74 AA;
                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                          11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                              07-AUG-2003
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                                                                                                                                                                                                                                                     ADG98744;
                                                                                                                                                                                                            RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VMDAVPARRWKE FVRTLGLREAE I EAVEVE I GRFRDQQYEMLKRWRQQQPAGLGAVYAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                           Apo-2 protein; apoptosis; cancer; tissue typing; transgenic animal; gene therapy; human; Apo-3/DR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Apo-2 polypeptides and encoding nucleic acid molecules, useful diagnosing, preventing or treating cancer, and in tissue typing or generating antibodies or transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
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100.0%; Pred. No. 5e-41;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim KJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chuntharapai A,
ADO40453 standard; protein; 74 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW93610 standard; protein; 65 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 2B; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-1997; 97US-0046615P.
09-FEB-1998; 98US-0074119P.
14-MAY-1998; 98US-00079029.
02-NOV-2001; 2002US-00257798.
06-NOV-2002; 2002US-00288917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-APR-2003; 2003US-00423448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74
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                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams CW, Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERMGLDGCVEDLRS
                                                                                                                                                                Human Apo-3/DR3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERMGLDGCVEDLRS
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ID AAWS
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AC AAWS
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AAW93610

1 VMDAVPARRWKEFVRTLGLREAEIEAVEVGRFRDQQYEMLKRWRQQQPAGLGAVYAAL 60

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(first entry)
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65; Conservative
                                                                                                                                                                                                                              Yu G,
                                                               osteoprotegerin; DR3
                                                                                                                                                                                                                                                   WPI; 2000-594575/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73
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                                                                                                                                                                                                                              Ni J, Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 65 AA;
                                                                                                          WO200056862-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 VEDLR
                                                                                     Homo sapiens
                                                                                                                                                                         24-MAR-1999;
                                                                                                                                                                                   14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-NOV-2002
                                                                                                                                                                                                                                                                                                         and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG31493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
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  원
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                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel human adriamycin-inducible killer protein located on chromosome 8p21, which also has p53-inducible, apoptosis-mediating activity and comprises an amino-terminal extracellular receptor, transmembrane and death domains. The nucleic acid molecule which encodes the protein, it's encoded signal transduction protein and antibodies of the invention are useful in the diagnosis and treatment of neoplastic diseases. The invention is also useful for the
                                                                                                                                                                                                                                                                                                                            A new nucleic acid encodes a p53-induced protein (Killer) - which induces apoptosis and is useful in the diagnosis and treatment of neoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                  Killer protein; adriamycin inducible; human; chromosome 8p21; diagnosis; p53-inducible; apoptosis-mediating activity; treatment; animal model; neoplastic disease; DR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, tumour necrosis factor, TNF, TR9 receptor, immunosuppressive,
antiinflammatory; cardiant, antiasthmatic, antidiabetic, antiallergic,
antiathritic, antirheumatic, anti-HIV, anticonvulsant, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.8%; Score 338; DB 2; Length 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No. 1.5e-35; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 46; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      production of animal model systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB26990 standard; protein; 65 AA.
                                                                                                                                                                                            97US-0054710P.
97US-0060473P.
98US-0077526P.
98US-0077628P.
                                                                                                                                                              98WO-US014495
                                                                                                                                                                                   97US-0052305P
                                                                                                                                                                                                                                        98US-0077661P
                               Human DR3 protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-FEB-2001 (first entry)
                                                                                                                                                                                                                                                             (UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human DR3 death domain.
                                                                                                                                                                                                                                                                                                        WPI; 1999-120857/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VEDLR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEDLR 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 65 AA;
                                                                                              Homo sapiens
                                                                                                                  WO9902653-A1
                                                                                                                                                                                                       30-SEP-1997;
11-MAR-1998;
11-MAR-1998;
                                                                                                                                                              10-JUL-1998;
                                                                                                                                        21-JAN-1999.
                                                                                                                                                                                                                                                                                 El-Deiry WS;
                                                                                                                                                                                            04-AUG-1997
                                                                                                                                                                                                                                        11-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                   diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB26990
ID AAB2
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AC AAB2
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The present sequence is the death domain of DR3. It was used for comparison to a domain of a novel human tumour necrosis factor receptor, designated TR9. The TR9 receptor is also known as Death Domain Containing Receptor 6. TR9 polypeptides, polymuclectides or agonists are useful for treating, preventing or diagnosing common variable immunodeficiency, X-linked agammaglobulinaemia, severe combined immunodeficiency and Wiskott-Aldrich syndrome, autoimmune diseases (such as rheumatoid arthritis, allergic encephalomyelitis, multiple sclerosis, diabetes mellitus and asthma), HIV infection, epilepsy, cancer, cardiovascular diseases and other neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid molecule encoding a human tumor necrosis factor receptor, known as TR9, useful for treating, preventing and diagnosing severe combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
                                                                                             autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis; multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer; cardiovascular disease; neurological disease; protein coordinate data;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RWKEFVRTLGLREAEIBAVBVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALBRWGLDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 RWKEFVRTLGLREABIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
neuroprotective, gene therapy, Death Domain Containing Receptor common variable immunodeficiency, X-linked agammaglobulinaemia; severe combined immunodeficiency; Wiskott-Aldrich syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, Apo-2DCR, Apo-2 ligand; programmed cell death, apoptosis; neurodegenerative disease; autoimmune; inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 338; DB 3; Length op; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Apo-2DcR associated protein #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 4C; 220pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0126019P.
99US-0134220P.
                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAR-2000; 2000WO-US006831.
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(GETH ) GENENTECH INC.
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                        23-SEP-1996;
31-MAR-1997;
                                                                            Ashkenazi AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
             01-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADG98745;
                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG98745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                           polypeptides, designated Apo-20ck, and the polymucleotide sequences encoding them. Apo-20ck is capable of binding Apo-2 ligand and is useful for modulating programmed cell death or apoptosis in mammalian cells. Apo-20ck can be used to produce apo-20ck antibodies which are useful the rapeutically, and can cross-react with other receptors for Apo-2 ligand to block excessive apoptosis in neurodegenerative diseases, or to block potentially autoimmune or inflammatory effects. Apo-20ck antibodies are also useful in immunohistochemistry staining assays or diagnostic assays for Apo-20ck, e.g. detecting it's expression in specific cells, tissues or serum, and for the affinity purification of Apo-20ck from recombinant cell culture or natural sources. The present sequence is given in the Seq listing but is invention. Note: The present sequence is given in the Seq listing but is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated Apo-2DcR polypeptide useful for modulating apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
                                                                                                                                                                                                                                     present invention relates to the isolation of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; affinity; competitive-type receptor; binding assay; cancer cell; human; TNF receptor family; hTNFRI; death domain; cytostatic.
                                                                                                                         Kim KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                      77.5%; Score 155; DB 5; Length 78; Local Similarity 46.1%; Pred. No. 7e-12; Nes 35; Conservative 13; Mismatches 24; Indels
                                                                                                                         Chuntharapai A, Gurney A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Death domain of human TNFR1 (hTNFR1) protein.
                                                                                                                                                                                                               Disclosure; Page 37; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA49709 standard; protein; 78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2002; 2002US-00112793.
                                            21-JUN-2001; 2001US-00887879
                                                                 97US-0049911P
                                                                           98US-00096500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 YAALERMGLDGCVEDL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GRVLRDMDLLGCLEDI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                      Ashkenazi AJ, Baker KP,
                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                        WPI; 2002-697823/75.
                                                                                                                                                                                         mammalian cells.
US2002102706-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2002192729-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 78 AA;
                                                                 18-JUN-1997;
                                                                           12-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                  Wood WI;
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Matches
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The present invention relates to the isolation of a biologically active Apo-2 ligand inhibitor (Apo-211) or Apo-3, and the polymucleotide sequences encoding them. Apo-211 and Apo-3 are involved in apoptosis. The Apo-211 and Apo-211 and Apo-211 in affainty purification techniques, and in competitive-type receptor binding assays when labelled with radioiodine, enzymes or fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or inducing apoptosis in cancer calls, and thus have therapeutic utility. The present sequence represents the death domain of a human TNF receptor family protein. This sequence is compared with the death domain of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                           Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, o:
Apo-3 polypeptide which induces or stimulates apoptotic activity, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAV 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apo-2; apoptosis; diagnosis; tissue-specific typing; transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.5%; Score 155; DB 6; Length 78; 46.1%; Pred. No. 7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADG98745 standard; protein; 78 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 6, 53pp; English
                              96US-00710802.
97US-00828683.
96US-00625328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2002; 2002US-00288917.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAY-1997; 97US-0046615P.
09-FEB-1998; 98US-0074119P.
14-MAY-1998; 98US-00079029.
02-NOV-2001; 2001US-00052798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 YAALERMGLDGCVEDL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | ||:||:
61 GRVLRDMDLLGCLEDI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 46.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFR1 death domain protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Conservative
                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                        in diagnostic assays.
                                                                                                                                                                                                                                                             WPI; 2003-657226/62.
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in diagnosing, treating and preventing cancer, tissue typing, in generating antibodies and transgenic animals. The invention is also useful in gene therapy. The present sequence is human TNFR1 protein. This sequence is used in the exemplification of the invention
 polynucleotide capable of modulating apoptosis. The invention is useful
                                                                                                                                                                                                                                                 RESULT 10
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                                                                                                                                                                                                            요
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                                                                                                                                                                                                                                                                                    1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAV 56
                                                                                                                                                                                                                                                                                                The present invention provides novel Apo-2 protein and the nucleic acid encoding the protein. The invention is useful in inducing apoptosis in mammalian cancer cells. The invention is also useful in diagnostic procedures for tissue-specific typing and in generating transgenic animals that are useful in development and screening of reagents. The invention is also useful in gene therapy. The present sequence is TNPR1 (tumour necrosis factor receptor 1) death domain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides novel Apo-2 polypeptide and the encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                                                                              Gaps
                                            New Apo-2 polypeptide or its extracellular or death domain sequence, useful for modulating apoptosis in mammalian cancer cells or for generating transgenic or knockout animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apo-2 protein; apoptosis; cancer; tissue typing; transgenic animal; gene therapy; human; TNFR1; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Apo-2 polypeptides and encoding nucleic acid molecules, useful diagnosing, preventing or treating cancer, and in tissue typing or
                                                                                                                                                                                                                                                               4,
                                                                                                                                                                                                                                   37.5%; Score 155; DB 7; Length 78;
46.1%; Pred. No. 7e-12;
ive 13; Mismatches 24; Indels
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 Kim
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 Chuntharapai A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chuntharapai A,
                                                                                           Disclosure; Fig 2B; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                  ADO40454 standard; protein; 78 AA
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14-MAY-1998; 98US-00079029.
02-NOV-2001; 2001US-00052798.
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GRVLRDMDLLGCLEDI
                                                                                                                                                                                                                                               Local Similarity 46.1
hes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC
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                       WPI; 2003-897574/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human TNFR1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2004009552-A1
                                                                                                                                                                                                               Sequence 78 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JAN-2004
 Adams CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                         ADO40454;
                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                       AD04045
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CXSXLTTTXBXBXBXBXBXBXBXBXXXXXXXXCXCX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A new nucleic acid encodes a p53-induced protein (Killer) - which induces apoptosis and is useful in the diagnosis and treatment of neoplastic
                                                                                                                                                                    1 VVENVPPLRWKEFVRRLGLSDHEIDRLELQNGRCLREAQYSMLATWRRRTPRREATLELL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Killer protein; adriamycin inducible; human; chromosome 8p21; diagnosis; p53-inducible; apoptosis-mediating activity; treatment; animal model; neoplastic disease; TNFR-1.
                                                                                                                                         1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAV 56
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel human adriamycin-inducible killer
                                                                                              4
                                               8; Length 78;
                                                                                            24; Indels
                                            37.5%; Score 155; DB 8, 46.1%; Pred. No. 7e-12;
                                                                                         13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 46; 65pp; English.
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97US-0054710P.
97US-0060473P.
98US-0077526P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human TNFR-1 protein fragment
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                                                                                                                                                                                                                                                                                    GRVĽRDMDĽĽĠČĽEĎI 76
                                                                                                                                                                                                                                                                                                                                                                                                          AAW93612 standard; protein;
              57 YAALERMGLDGCVEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Sequence 78 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYPE-) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-Deiry WS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW93612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases.
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GAVYAALERMGLDGCVEDLRSRLQRGP 30

(first entry)

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AAB26989 standard; protein; 68 AA
                                                                                                                                            Human TNFR 1 death domain.
                                                                                                                   32-FEB-2001
                                                                                           AAB26989;
                                      RESULT 12
AAB26989
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                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production of other cyckines in other cell populations. The population of other cyckines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cyckkinelike activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, individual activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; archititis; inflammation.
                                                  9 RWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAVYAALERMG 64
                             4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 22587; 1399pp + Sequence Listing; English.
34.4%; Score 142; DB 2; Length 69; 47.1%; Pred. No. 2.8e-10; ive 11; Mismatches 21; Indels
                                                                                                                                                                                                                                                                   Human polypeptide SEQ ID NO 22587.
                                                                                                                                                                                          AA008695 standard; protein; 30 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2000; 2000US-00515126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAY-2000; 2000US-00577409
                                                                                                                                                                                                                                           06-NOV-2001 (first entry)
                          32; Conservative
                                                                                                                   | ||:||:
LLGCLEDI 68
                                                                                                    65 LDGCVEDL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 27; Conserv
             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAI88626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30 AA;
                                                                                                                                                                                                                                                                                                                                                                                    WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-2001
                                                                                                                                                                                                                   AAO08695;
 Query Match
              Local
                         Matches
                                                                                                                                                                  RESULT 11
AAO08695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecule encoding a human tumor necrosis factor receptor, known as TR9, useful for treating, preventing and diagnosing severe combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
Human; tumour necrosis factor; TNF; TR9 receptor; immunosuppressive; antiinflammatory; cardiant; antiasthmatic; antidiabetic; antiallergic; antiathritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic; neuroprotective; gene therapy; Death Domain Containing Receptor 6; common variable immunodeficiency; X-linked agammaglobulinaemia; severe combined immunodeficiency; Wiskott-Aldrich syndrome; autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis; multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer; cardiovascular disease; neurological disease; protein coordinate data;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 4C; 220pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fan P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAR-2000; 2000WO-US006831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0126019P.
99US-0134220P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 46.3%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ບັ
                                                                                                                                                                                                                                                                                           osteoprotegerin; TNFR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ni J, Gentz RL, Yu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-594575/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGCVEDL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LGCLEDI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 68 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                WO200056862-A1
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
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Gaps

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33.7%; Score 139; DB 4; Length 30; 100.0%; Pred. No. 2.5e-10; Live 0; Mismatches 0; Indels

54 GAVYAALERMGLDGCVEDLRSRLQRGP 80

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Conservative

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ADG42594 standard; protein; 75 AA.
                                                                                                                                                                                                                                                                                                                                                                           Herrmann JL, Rastelli L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in human NOV1 protein.
                                                                                                                                                                                                                                                                                                                   (HERR/) HERRMANN J L.
(RAST/) RASTELLI L.
(SHIM/) SHIMKETS R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 ALERMGLD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALRKWGRD 73
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-900673/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                         JS2003204052-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 75 AA;
                                                                                                                                                                               Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-2004
                                                                               26-FEB-2004
                                                                                                                                                                                                                                   30-OCT-2003.
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                                                     ADG42594;
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Best Local S
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RESULT 14
             ADG42594
                                        셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor (p55 TNF-R). The death domain of the p55 tumour necrosis factor receptor (p55 TNF-R). The death domain (DD) of human Fas-ligand receptor (FAS-R), ankyrin 1, nerve growth factor receptor (NGF-R) and MORT-I.

(which binds to the intracellular portion of (FAS-R)) are also given (see AAW00206-07 and AAW00209-W00210). These DDs are used to identify compounds capable of modulating activity of the regulatory proteins (p55, NGF, TNF and FAS-R ligand, WORT-I) via interaction with the DDs. Such modulators which may be antibodies, antiense sequences or ribozymes (which can affect the cellular mRNA sequences encoding the proteins) and are useful for modulation of effects of the regulatory proteins within the cell. Tumour cells, HIV-infected cells or other diseased cells can be treated by targeting the cells with animal viral vectors encoding the modulators and a viral surface antigen capable of binding to a specific receptor. The DDs are characterised by having groups of common amino acid residues Trp, Ala, Asp, Glu, Thr, Arg and Tyr within locations that can be aligned to show homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modulator of regulatory cellular events mediated by "death domain" contg. regulatory proteins - useful for modulating functions mediated in cells by proteins contg the death domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 WKEFVRRIGLSDHEIDRLELQNGRCLREAQYSMLATWRRRTPRR----EATLELLGRVLR 56
                                                                                                                                               Death domain; regulatory protein; NGF-R; nerve growth receptor; FAS-R; Fas ligand receptor; Fas/APO1; ankyrin 1; D55 TNF-R; tumour necrosis factor receptor; MORT1; cell cytoxicity; HIV; human immunodeficiency virus; cancer; neoplasia; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 WKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQPAGLGAVYAALERMG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.6%; Score 118; DB 2; Length 64;
42.6%; Pred. No. 3.2e-07;
iive 10; Mismatches 17; Indels 12; Gaps
                                                                                                                      Human p55 tumour necrosis factor receptor death domain motif.
                                                                                                                                                                                                                                                                                                                                                                                                                    Mett I;
                                                                                                                                                                                                                                                                                                                                                                                                                  Pancer Z,
                                                                                                                                                                                                                                                                                                                                                                                                                  Varfolomeev EE,
                                     AAW00208 standard; peptide; 64 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; Fig 1; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                          (YEDA ) YEDA RES & DEV CO LTD. (WEIN/) WEINWURZEL H.
                                                                                                                                                                                                                                                                                                                                 95IL-00112742.
                                                                                                                                                                                                                                                                                                                                                95IL-00115289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 42.6%
Matches 29; Conservative
                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  Boldin MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---LDGCV 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-402125/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 64 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Soncharov TM;
                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                WO9625941-A1
                                                                                                                                                                                                                                                                                                                                   22-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                13-SEP-1995;
                                                                                                                                                                                                                                                                          29-AUG-1996.
                                                                                           16-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                  Wallach D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57
                                                               AAW00208;
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The invention describes a new isolated polypeptide comprising: a polypeptide or its mature form comprising a sequence not given in the specification; or a variant of (A), where one or more amino acid residues in the variant differs in no more than 15% from the amino acid sequence of the mature form. The pharmaceutical composition may be administered via oral, transdermal, rectal or parenteral route. The polypeptide, nucleic acid or antibody is useful for preparing a composition for treating or preventing a NOVX-associated disorder, e.g., cancer. This is the amino acid sequence of a protein associated with analysis of domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LLDDPLGRDWRRLARKLGLSEEEDQIEHENPRLASPTYQLLDIWEQRGGKNATVGTLLE 65
                                                                  cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical; NOVX-associated disorder; cancer; NOVX; domain analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New NOVX gene or NOVX-specific antibody, useful for preparing a composition for treating or preventing a NOVX-associated disorder, e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQ--QPAGLGAVYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30; Indels
NOV1 domain analysis associated protein seq id 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.4%; Score 105; DB 7; 35.3%; Pred. No. 1.8e-05; iive 12; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 47; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimkets RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AD040451 standard; protein; 76 AA.
                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2001; 2001US-00970944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-OCT-2000; 2000US-0237862P.
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2; Gaps

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61 ERMG 64 | :| 63 ETLG 66

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Search completed: June 27, 2005, 14:37:58 Job time : 160 secs

3 DAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDOOYEMLKRW--ROOOPAGLGAVYAAL

Query Match 22.8%; Score 94; DB 8; Length 76; Best Local Similarity 34.4%; Pred. No. 0.00049; Matches 22; Conservative 11; Mismatches 29; Indels

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1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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US-09-887-879-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.5
63
60

    COUNTY    C
                                                                                                                                                                                                                                                                                                         70.5
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Best Local S:
Matches 74
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ORGANISM:
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Sequence 16, Appl
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Sequence 16, Appl
Sequence 23, Appl
Sequence 21, Appl
                                                                                                                                                                                       June 27, 2005, 14:38:10 ; Search time 163 Seconds (without alignments) 188.735 Million cell updates/sec
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1: /cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.Pep:*
2: /cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.Pep:*
3: /cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.Pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-922-964-15
US-10-207-295-9
US-10-242-383-15
US-09-756-854-24
US-10-041-574-24
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Maximum Match 100%
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Perfect score:
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Gaps ö

92.3%; Score 381; DB 9; Length 74; 100.0%; Pred. No. 1.2e-38; ive 0; Mismatches 0; Indels

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Sequence 3, Appli
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       US-09-756-854-23

3 US-10-031-40-23

3 US-10-035-408-3

4 US-10-207-295-7

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4 US-10-041-574-26

5 US-10-041-574-26

6 US-10-041-574-26

6 US-10-037-996-26

7 US-10-207-295-8

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6 US-10-041-574-25

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9 US-10-042-59-118

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US-10-040-862-721
US-10-057-475B-721
US-10-154-884B-721
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US-09-992-964-17
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61 ERMGLDGCVEDLRS 74

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ERMGLDGCVEDLRS 74

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PRIOR APPLICATION DATA:
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                             APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin
APPLICANT: Baker, Kevin
APPLICANT: Gurney, Austin
APPLICANT: Wood, William
ITILE OF INVENTION: Apo-2DCR
FILE REFERENCE: P1110
CURRENT APPLICATION NUMBER: U8/09/992,964
CURRENT APPLICATION NUMBER: 08/878,168
PRIOR FILING DATE: 1997-06-18
NUMBER: OF SEQ ID NOS: 17
LENGTH: 74
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COS-10-20-5

Publication No. US20030017161A1

GERREAL INFORMATION:

APPLICANT: Ankenazi, Avi J.

APPLICANT: Chuntharapai, Anan

APPLICANT: Kim, Kyung Jin

CURRENT APPLICATION NUMBER: US/10/207.295

CURRENT FILING DATE: 1998-02-09

PRIOR PELICATION NUMBER: US/09/020,746

                                                                                                                                   US-09-992-964-15

Sequence 15, Application US/0992964

; Setent No. US20020161202A1

; GENERAL INFORMATION:
ERMGLDGCVEDLRS 74
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Matches 74; Conservative
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ORGANISM: Homo sapiens
US-09-992-964-15
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ORGANISM: Homo sapiens
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Yu, Guo-Liang
Pan, Ping
Gent, Reiner
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
92.3%; Score 381, DB 14;
Best Local Similarity 100.0%; Pred. No. 1.2e-38;
Matches 74; Conservative 0; Mismatches 0;
                                                                                                                           APPLICANT: Baker, Kevin P.
APPLICANT: Chuntharapai, Anan
APPLICANT: Curney, Austin
APPLICANT: Wood, William I.
TITLE OF INVENTION: Apo-2DCR
FILE REFERENCE: P1110P1
CURRENT APPLICATION NUMBER: US/10/242,383
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/10/242,383

PRIOR PLING DATE: 2002-09-11

PRIOR FILING DATE: 2001-06-21

PRIOR PLILING DATE: 2001-06-21

PRIOR APPLICATION NUMBER: 09/096,500

PRIOR PILING DATE: 1998-06-12

PRIOR PILING DATE: 1997-06-18

PRIOR PILING DATE: 1997-06-18

SEQ ID NO 15

LENGRIH: 74

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APPLICATION NUMBER: US/09/756,854
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CLASSIFICATION: <Unknown>
US-10-242-383-15
; Sequence 15, Application US/10242383
; Publication No. US20030138915A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 24, Application US/09756854; Patent No. US20020164684A1; GENERAL INFORMATION:
                                                                                                       APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ERMGLDGCVEDLRS 74
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-834-966-24
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RWKEFVRTLGLREAEIEAVEVGIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 RWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24, Application US/10041574
Publication No. US20020168359A1
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Fan, Ping
APPLICANT: Fan, Ping
APPLICANT: Fan, Ping
APPLICANT: Fan, Fing
FILE REFERENCE: PF375P1
FILE REFERENCE: PF375P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
81.8%; Score 338; DB 9; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 65; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE KEFEKENCE: F43.75TL
CURRENT APPLICATION NUMBER: US/10/041,574
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: 09/527,236
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATCHTIN VET. 2.1
SOFTWARE: PATCHTIN VET. 2.1
                                                             NAME: HOOVET, KENIEW K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF375
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 65 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 24: US-09-756-854-24
APPLICATION NUMBER: 09/095,094
                          FILING DATE: <Unknown:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: Homo sapiens
US-10-041-574-24
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US-10-207-295-10
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LENGTH: 78
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                                                                                                                                   1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAV 56
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; Publication No. US20020192729A1
; Publication No. US20020192729A1
; FURLICANTION:
; TITLE OF INVENTION: APO-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Genentech, Inc.
STREET: 1 DNA WAY
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.5%; Score 155; DB 9; Length 78; llarity 46.1%; Pred. No. 5e-11; Conservative 13; Mismatches 24; Indels
                                   37.5%; Score 155; DB 9; Length 78;
46.1%; Pred. No. 5e-11;
tive 13; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATE:
FILING DATE: 28-Mar-2002
                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/09992964
; Betten No. US20020161202A1
; GENERAL INFORMATION:
; APPLICANT: ABINEmazi, Avi J.
; APPLICANT: Baker, Kevin
; APPLICANT: Baker, Kevin
; APPLICANT: Baker, Kevin
; APPLICANT: Wood, William
; TILE OF INVENTION: Apo-2DCR
; FILE REFERENCE: P1110
CURRENT APPLICATION WUMBER: US/09/992,964
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 08/878,168
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 78
                                                                                                                                                                                                             61 GRVLRDMDLLGCLEDI 76
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                                                                                                                                                                                        57 YAALERMGLDGCVEDL 72
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                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-992-964-16
                               Query Match
Best Local Similarity
Matches 35; Conserv
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Best Local Similarity
Matches 35; Conserv
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US-09-887-879-16
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1 UMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAV 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.5%; Score 155; DB 13; Length 78; 46.1%; Pred. No. 5e-11; tive 13; Mismatches 24; Indels
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46.1%; Pred. No. 5e-11;
tive 13; Mismatches 24; Indels
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
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Sequence 10, Application US/10207295

Publication No. US20030017161A1

GENERAL INFORMATION:
APPLICANT: Abhkenal, Avi J.
APPLICANT: Kim, Kyung Jin
TITLE OF INVENTION: APO-2 RECEPTOR
FILE REFERENCE: 11669-28US04

CURRENT APPLICATION NUMBER: US/10/207,295

CURRENT FILING DATE: 1998-02-09

PRIOR APPLICATION NUMBER: US/09/020,746

PRIOR APPLICATION NUMBER: US/09/020,746

PRIOR FILING DATE: 1998-02-09

PRIOR FILING DATE: 1997-05-15

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                         FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REFERENCE/DOCKET NUMBER: 95,600
REFERENCE/DOCKET NUMBER: P1007P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                  FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-892-1996
APPLICATION NUMBER: 08/710802
                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 78 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 YAALERMGLDGCVEDL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GRVLRDMDLLGCLEDI 76
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Matches 35; Conservative
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Gaps

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1 RWKEFVRRIGISDHEIDRIELQNGRCLREAQYSMLATWRRTRREATLELIGRVLRDMDL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 RWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQ--QQPAGLGAVYAALERMGL
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APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Fan, Ping
APPLICANT: Fan, Ping
APPLICANT: Fan, Ping
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REFERENCE: PF375P1
CURRENT APPLICATION NUMBER: US/10/041,574
CURRENT FILING DATE: 2002-01-10
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 09/527,236
PRIOR APPLICATION NUMBER: 09/529,991
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 27
SEQ ID NOS: 27
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.1%; Score 136.5; DB 13; Length 68; Best Local Similarity 46.3%; Pred. No. 7.7e-09; Matches 31; Conservative 12; Mismatches 21; Indels 3
                                                                                                                                                                                                                                                                                                                                                       Length 68;
                                                                                                                                                                                                                                                                                                                                                                                                     21; Indels
                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                                                  Query Match 33.1%; Score 136.5; DB 9
Best Local Similarity 46.3%; Pred. No. 7.7e-09;
Matches 31; Conservative 12; Mismatches 21
                                                                                                                                                                                                         // TOPOLOGY: linear
// MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-756-854-23
                   REFERENCE/DOCKET NUMBER: PF375
TELECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23, Application US/10041574
Publication No. US20020168359A1
GENERAL INFORMATION:
                                                                  TELEPHONE: 301-309-8504
                                                                                   TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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61 LGCLEDI 67
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61 LGCLEDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fan, Ping
Gentz, Reiner
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCE: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.5%; Score 155; DB 14; Length 78;
46.1%; Pred. No. 5e-11;
tive 13; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPLING DATE: 10-Jan-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                    APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Chuntharapai, Anan
APPLICANT: Chuntharapai, Anan
APPLICANT: Gurney, Austin
APPLICANT: Kim, Kyung Jin
APPLICANT: Kim, Kyung Jin
APPLICANT: Wood, William I.
TITLE OF INVENTION: Apo-2DCR
FILE REFERENCE: P1110P1
CURRENT APPLICATION NUMBER: US/10/242,383
CURRENT APPLICATION NUMBER: US/09/887,879
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-06-21
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-12
PRIOR PILING DATE: 1998-06-18
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 16
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PRIOR APPLICATION NUMBER: 09/095,094
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
              5.10-242-383-16
Sequence 16, Application US/10242383
Publication No. US20030138915A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23, Application US/09756854 Patent No. US20020164684A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hoover, Kenley K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ni, Jian
Yu, Guo-Liang
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61 GRVLRDMDLLGCLEDI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 YAALERMGLDGCVEDL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 37.5
Best Local Similarity 46.1
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-756-854-23
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65 9

Gaps

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### Sequence 23, Application US/10834966

| Sequence 23, Application US/10834966
| Publication No. US20040197070A1
| GENERAL INFORMATION:
| APPLICANT: Wi, Jun. Linn
| APPLICANT: Fan, Ping
| Fing APPLICATION WINGER: US/10/041,574
| FING RAPLICATION WINGER: US/200-03-16
| FING RELING DATE: 2000-03-16
| FING RELING DATE: 2000-03-16
| FING RELING DATE: 1999-06-10
| FING RELING DATE: 1999-06-10
| FING RELING DATE: 1999-06-14
| FING PILING DATE: 1999-06-14
| FING RELING DATE: 1999-06-14
| FIN
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66 DGCVEDL 72 ||:||: 61 LGCLEDI 67

g &

Search completed: June 27, 2005, 14:53:23 Job time : 164 secs

21, Appl 21, Appl 10142, A 3076, Ap 3335, Ap 3730, Ap 3898, Ap

, Appli 122, Ap Appli

Sequence Seq

24, Appl 2, Appli 27, Appl

Appli Appli

Sequence Sequence Sequence

Sequence

Н

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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1 RWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 RWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGC
                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-527-236A-24

i Sequence(24) Application US/09527236A

j Patent No. 6386508

GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: To Guo-Liang
APPLICANT: To Guo-Liang
APPLICANT: Gentz, Reiner L.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
TITLE OF INVENTION NUMBER: US/09/52,991
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1998-06-10
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS-22

NUMBER OF SEQ ID NOS-22

SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 24

LENGTH: 65

LENGTH: 65

LENGTH: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.8%; Score 338; DB 3; Length 65; 100.0%; Pred. No. 6.2e-37; ive 0; Mismatches 0; Indels
             US-09-756-854-25
US-09-156-87A-5
US-08-818-618-24
US-08-818-618-24
US-08-818-618-24
US-08-134-626-2
US-09-134-001C-5122
US-09-134-001C-5122
US-09-134-001C-3135
US-09-134-001C-3135
US-09-134-001C-3135
US-09-134-001C-3135
US-09-134-001C-3135
US-09-134-001C-31898
US-09-134-001C-31898
US-09-134-001C-31898
US-09-134-001C-31898
US-09-134-001C-31898
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Patent No. 6667390
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
Fan, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 100.
65; Conservative
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ORGANISM: Homo sapiens
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 US-09-527-236A-24
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Query Match
Best Local S
Matches 65
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Sequence 24, Appl
Sequence 24, Appl
Sequence 6, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 11, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 25, Appli
Sequence 24, Appli
Sequence 24, Appli
Sequence 24, Appli
Sequence 27, Appli
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Sequence 118, App
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Sequence 1, Appli
                                                                                                                        June 27, 2005, 14:32:34; Search time 43 Seconds (without alignments) 138.882 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                          1 VMDAVPARRWKEFVRTLGLR......BRMGLDGCVEDLRSRLQRGP
                                                                                                                                                                                                                                                                                                                                                                           307244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued Patents AA:*
1: /cgn2_6/ptodata1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata1/iaa/6B_COMB.pep:*
6: /cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-444-005-29
US-09-069-827A-118
US-08-995-050-1
US-08-219-237B-10
US-08-894-626-1
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US-09-756-854-24
US-09-159-277A-6
US-09-159-277A-6
US-09-247-236A-23
US-09-756-854-25
US-09-756-854-26
US-08-844-628-28
US-09-756-854-26
US-09-57-236A-26
US-09-57-236A-26
US-09-57-236A-26
US-09-95-159-7
US-08-95-159-7
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                                                                                                                                                                                                                                                                                                                                    513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                        US-10-081-280-6_COPY_338_417
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Maximum Match 100%
Listing first 45 summaries
                                                                                           protein search, using sw model
                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0 Maximum DB seq length: 80
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Gaps

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9

60 59 57.5 57.5

65.5

338 338 155 142 142 136.5 136.5

Score

Result No.

73.5 70.5 70.5

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FILING DATE: 31-Mar-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                   TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 78 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                         TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 YAALERMGLDGCVEDL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | ||:||:
61 GRVLRDMDLLGCLEDI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-828-683A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-159-277A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 RWKEFVRTLGLREAEIEAVEVEIGRFRDQQYEMLKRWRQQQPAGLGAVYAALERMGLDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                  TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                 COMPUTER: IEAM PC COMPATIBLE
COMPUTER: IEAM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,854
FILING DATE: 10-Jan-2001
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION OF THE COMPATA:
APPLICATION NUMBER: 09/095,094
FILING DATE: CURROWN>
ATTORNEY/AREN INFORMATION:
NAME: HOOVEY, Kenley K.
REFERENT INFORMATION:
REFERENCE/DOCKET NUMBER: PF3.75
TELECOMMUNICATION NUMBER: PF3.75
TELECOMMUNICATION NUMBER: PF3.75
TELECHONE: 301-309-8504
NUMBER: STENT NOWNATION:
TELEFAK: 301-309-8449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

81.8%; Score 338; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 6.2e-37;
Matches 65; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ashkenazi, Avi J.
TILE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-756-854-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Application US/08828683A Patent No. 6469144 GENERAL INFORMATION:
                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 65 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
Gentz, Reiner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                           ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                              CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 VEDLR 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAV 56
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Sequence 6, Application US/09159277A
GENERAL INFORMATION:
APPLICANT: DIXIV. VISHVA M.
APPLICANT: O'ROURKE, KAREN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING
TITLE OF INVENTION: ASSOCIATED APOPTOSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.5%; Score 155; DB 4; Length 78; 46.1%; Pred. No. 7.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,277A
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: MARSE/ABCSTATION NUMBER: 35,600
REFERENCE/POCKET NUMBER: 91007P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442107001
TELECOMUNICATION INFORMATION:
TELEPHONE: (650)813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/844,691
FILING DATE: 21-APR-1997
APPLICATION UNDERF: US 08/416,379
FILING DATE: 03-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Morrison & Foerster LLP
755 Page Mill Road
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JS-09-527-236A-23
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                                                                                                                                                             Query Match
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Matches
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 RWKEFVRTLGLREAEIEAVEVEIGR-FRDQOYEMLKRWRQQQP---AGLGAVYAALERMG 64
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: DIXII, VISHVA M.
APPLICANT: DIXII, VISHVA M.
APPLICANT: O'ROUNEE, KAREN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING
TITLE OF INVENTION: PAS-ASSOCIATED APOPTOSIS
NUMBER OF SEQUENCES:
ADDRESSE: MORTISON & FOSTSTER LLP
                                                                                                                                                                                                                                                                                                                                                         Query Match 34.4%; Score 142; DB 4; Length 70; Best Local Similarity 47.1%; Pred. No. 3.4e-11; Matches 32; Conservative 11; Mismatches 21; Indels
                                                                                                                                                                                                                                            LOCATION: 11

OTHER INFORMATION: /note= "Leu is replaced by Asn for other INFORMATION: the point mutant hTNFR-1"
US-09-159-277A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIN RC-BCS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,691A
FILING DATE: 21-APR-1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/416,379
FILING DATE: 03-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: KORBKI, ARLOIMERE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442107001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08844691A
Patent No. 6747138
TELEFAX: (650)494-0792
TELEX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (650)494-0792
TELEX: 706141 MRSNFORRS SFO
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 amino acids
                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ||:||:
61 LLGCLEDI 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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1 RWKEFVRRLGLSDHEIDRLELQNGRCLREAQYSMLATWRRTFRREATLELLGRVLRDMD 60
                                                                                                                                                                                                                                                              9 RWKEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP---AGLGAVYAALERMG
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Gentz, Reiner
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | JAPPLICANT: Ni, Jian |
| APPLICANT: Ni, Guo-Liang |
| APPLICANT: Fan, Ping |
| APPLICANT: Fan, Ping |
| APPLICANT: Fan, Ping |
| APPLICANT: Gentz, Reiner L. |
| TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9 |
| FILE REFERENCE: PE375P1 |
| CURRENT APPLICATION NUMBER: US/09/527,236A |
| CURRENT FILING: DATE: 2000-03-16 |
| PRIOR PLILING DATE: 1997-06-11 |
| PRIOR FILING DATE: 1999-06-11 |
| PRIOR PLILING DATE: 1999-03-24 |
| PRIOR FILING DATE: 1999-05-14 |
| NUMBER OF SEQ ID NOS: 27 |
| SEQ ID NO 23 |
| LENACTH: 6A
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                                                                                                                                                    y Match 34.4%; Score 142; DB 4; Length 70; Local Similarity 47.1%; Pred. No. 3.4e-11; hes 32; Conservative 11; Mismatches 21; Indels
NAME/KEY: Modified-site
| NAME/KEY: Modified-site
| LOCATION: 11
| OTHER INFORMATION: /note= "Leu is replaced by Asn for OTHER INFORMATION: the point mutant hTNFR-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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46.3%; Pred. No. 1.7e-10;
tive 12; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23, Application US/09527236A Patent No. 6358508 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 23, Application US/09756854; Patent No. 6667390; GENERAL INFORMATION:
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Yu, Guo-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 46.3
nes 31; Conservative
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CORGANISM: Homo sapiens
US-09-527-236A-23
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61 LLGCLEDI 68
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61 LGCLEDI 67
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 RWKEFVRTLGLREAEIEAVEVEIGR-FRDQOYEMLKRWRQ--QQPAGLGAVYAALERMGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.1%; Score 136.5; DB 4; Length 68; 46.3%; Pred. No. 1.7e-10; tive 12; Mismatches 21; Indels
                                                                                                                         ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,854
FILING DATE: 10-Jan-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METT, Igor
GONCHAROV, Tanya M.
WEINTRIZEL, Henry
TITLE OF INVENTION: MODULATORS OF REGULATORY PROTEINS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C. STREET: 419 Seventh Street N.W., Ste. 300 CITY: Washington
                   ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/095,094
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
NAME: HOOVET, KENLEY K.
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PF375
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08894626
Patent No. 6355780
GENERAL INFORMATION:
APPLICANT: WALLACH, David
BOLDIN, Mark P.
VARFOLOMEEV, Eugene E.
PANCER, Zeev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
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COUNTRY: USA
ZIP: 20004
                                                                                                            COUNTRY: US
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61 LGCLEDI 67
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1 WKEFVRRIGISDHEIDRIELGNGRCIREAQYSMLATWRRRTPRR----EATLELLGRVIR 56
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Patent No. 5874546
GENERL INFORMATION:
APPLICANT: NAGATA, Shigekazu
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: James W. Hellwege
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.6%; Score 118; DB 3; Length 64; 42.6%; Pred. No. 4.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Mismatches 17; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                  CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/08/894,626
FILING DATE: 09-Dec-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 112,742
FILING DATE: 22-FEB-1995
APPLICATION NUMBER: IL 115,289
FILING DATE: 13-SEP-1995
APPLICATION NUMBER: PCT/US96/02326
FILING DATE: 13-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY: ROGET.
REFERENCE/DOCKET NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
TELEPHONE: (202) 1717-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-894-626-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: James W. Hellwege
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/219,237B
FILING DATE: 28-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,129
FILING DATE: 22-APR-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 64 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 ---LDGCV 69
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Matches 29; Conserva
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US-08-444-005-28
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                                                                                                                                                                                                                                                                                                                                 Gaps
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Gentz, Reiner
IITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
NUMBER OF SEQUENCE: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yu, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Yu, Guo-Liang
APPLICANT: Pang
APPLICANT: Gentz, Refiner L.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
FILE REFERENCE: PF375P1
CURRENT APPLICATION HUMBER: US/09/527,236A
CURRENT FILING DATE: 2000-03-16
FRIOR FILING DATE: 1997-06-11
FRIOR APPLICATION NUMBER: 09/095,094
FRIOR PILING DATE: 1998-06-10
FRIOR APPLICATION NUMBER: 60/126,019
FRIOR PILING DATE: 1999-06-14
FRIOR FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                               Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.1%; Score 83; DB 3; Length 67; 33.3%; Pred. No. 0.0018; tive 11; Mismatches 25; Indels
                                                                                                                                                                                                                                                                          Score 102.5; DB 2; Length
Pred. No. 2.9e-06;
8; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            1 KEFVRRIGLSDHEIDRLELQNGRCLREAQYSMLATWRRTP 41
                                                                                                                                                                                                                                                                                                                                                                               11 KEFVRTLGLREAEIEAVEVEIGR-FRDQQYEMLKRWRQQQP 50
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STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/09527236A Patent No. 6358508 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/09756854
Patent No. 6667390
GENERAL INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 516
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                             24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ni, Jian
Yu, Guo-Liang
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 51.2%
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                 TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-219-237B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 19; Conserv
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COMPUTER: PRADALE FORM:

COMPUTER: PRADALE FORM:

COMPUTER: INH PC COMPARILIDE

APPLICATION NUMBER: 10,03756,854

FILLING DATE: IN-10,03709/756,854

MARCHA PRESENTE: IN-10,03709/756,854

OM VINERANIENCE TARE FORDER: IN-10,03709/756,854

OM VINERANIENCE TARE: IN-10,03709/756,854

FRESULT 12

GENERAL IN-10,03709/756,854

COMPUTER: BARANIE SECUENCES: 35

COMPUTER: BARANIE SECUENC
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7 KHWKNCARKLGFTQSQIDEIDHDYERDGLKEKVYQMLQKWVMREGIKGATVGKLAQALHQ 66
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Patent No. 6495322
GENERAL INPORMATION:
APPLICANT: Ni, Jian
TITLE OF INVENTION: RAIDD, A No. 6495322el Death Adaptor Molecule
FILE REPRENCE: 1488.0860002
CURRENT APPLICATION NUMBER: US/09/545,605
CURRENT FILING DATE: 2001-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
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                                                                                                                                                         Sequence 27, Application US/08828683A
Patent No. 6469144
GENERAL INFORMATION: Abhkenazi, Avi J.
TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRET APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
CLASSIPICATION OF CURROWN: APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-589-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-08-828-683A-27
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PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60,033,868
PRIOR FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 77 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 25.0%
Watches 15; Conservative
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                                                                                                                                     US-08-828-683A-27
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 73.5; DB 1; Length 41;
Pred. No. 0.017;
7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08995159

Requent No. 6130079

GENERAL INFORMATION:
APPLICANT: DIXIT, VISHVA M.
APPLICANT: DIXIT, VISHVA M.
TITLE OF INVENTION: RAIDD, A NOVEL DEATH ADAPTOR MOLECULE NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: MACHINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.1%; Score 70.5; DB 3; Length 77; 25.0%; Pred. No. 0.091; tive 19; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,159
FILING DATE: Herewith
CLASSIFFFFFFFF
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,868
FILING DATE: 20-DEC-1996
CLASSIFICATION:
NAME: GOLOSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1488.086001
TELEPONINICATION INFORMATION:
TELEPONINICATION INFORMATION:
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                                                                                                                                                                                   LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                    TELEX: 200154
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 48.4%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                   TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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                                                                                                                                                                                                                                                                                                               / MOLECULE TYPE: protein US-08-444-005-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 15; Conserva
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                                                                    TELEFAX:
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; SEQ ID NO 7
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-545-605-7
Query Match
US-09-545-605-7
Query Match
Best Local Similarity 25.0%; Pred. No. 0.091;
Matches 15; Conservative 19; Mismatches 21; Indels 5; Gaps 2;
Matches 15; Conservative 19: Mismatches 21; Indels 5; Gaps 2;
OY

8 RRWKEFVRIGEREAEIEAVEVEIGR--FRDQQYEMLKRWRQQQ---PAGLGAVYAALER 62
DD
7 KHWKNCARKLGFTQSQIDEIDHDYERDGLKEKVYQMLQKWVMREGIKGATVGKLAQALHQ 66
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Search completed: June 27, 2005, 14:42:24 Job time : 44 secs

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